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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-133-2

US-08-290-133-2

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APPLICANT: THEILL, LARS EYDE APPLICANT: YU, GANG TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
                                                                                                                                                                                                          61 LIISLAVFVLMFILIRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR PELING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                                                                                                                121 EECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 180
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                                                                                                                                    1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
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Query Match 98.5%; Score 950; DB 4; Length 181; Best Local Similarity 100.0%; Pred. No. 4e-102; Matches 181; Conservative 0; Mismatches 0; Indels
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Patent No. 6475987
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; Sequence 11, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
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Matches 117; Conserva
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                                                                                                                                             TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND TITLE OF INVENTION: METHODS OF USE THEREOF FILE REPRENCE: 2879-72
CURRENT PAPLICATION NUMBER: US/09/565,423
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PARENTIN VET: 2.1
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
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100.0%; Score 964; DB 4; Length 184;
Best Local Similarity 100.0%; Pred. No. 9.8e-104;
Matches 184; Conservative 0; Mismatches 0; Indels
                                              ALIGNMENTS
                                                                                                                                    Detente 11, Application US/09565423
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SOFWARE: Patentin version 3.1
SEQ ID NO 5
LENGTH: 181
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; ORGANISM: Homo sapiens
US-09-854-864-5
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APPLICANT: THEILL, LARS EYDE
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APPLICANT: THEILL, LARS HODE
APPLICANT: TYU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 12
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 AVFVLMFILLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTC 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AQCBYPDSLLHAC-PC-LRCS----PPTCQ-YC--SVT-SVKGT---LM--LGL---LSL 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.3%; Score 311.5; DB 4; Best Local Similarity 61.5%; Pred. No. 2.7e-28; Matches 96; Conservative 4; Mismatches 7;
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Sequence 9, Application US/09854864
Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: human-murine Consensus
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Matches 80; Conserv
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| Sequence 21, Application US/09854864
| Sequence 21, Application US/09854864
| Sequence 21, Application US/09854864
| Patent No. 6774106
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EYDE
| APPLICANT: TYU, GANG
| TITLE OF INVENTION WETHOOS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
| TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-6868
| CURRENT APPLICATION NUMBER: US/09/854,864
| CURRENT FILING DATE: 2000-05-12
| PRIOR PILING DATE: 2000-05-12
| PRIOR PLING DATE: 2000-06-27
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAQQCFHSEYPDSLIAACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
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FILE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-68GB
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT TILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
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Best Local Similarity 62.64
Matches 117; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Murine
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US-09-854-864-12
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LENGTH: 58
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Best Local
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Gaps

49;

Indels

DB 4; Length 117;

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GENERAL INC. 0'.1910B
GENERAL INC. 0'.1910B
GENERAL INFORMATION:
APPLICANT: THERLL, LARS EYDE
APPLICANT: THERLL, LARS EYDE
APPLICANT: YU, GANG
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT PILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VETSION 3.1
SEQ ID NOS: 31
SEQ ID NOS: 31
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77 EDC-KSKPK-DSDH-FPLPAMEEGATILVTTKT-DY 108
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1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34

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GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: TU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: METHODS AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SCOTWARRE: PATENTIN VERSION 3.1
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SED ID NOS: 31
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                                                                                                                     Sequence 13, Application US/09854864
Patent No. 6774106
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ORGANISM: Consensus
                                                                                                 US-09-854-864-13
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LENGTH: 281
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-17
PRIOR FILING DATE: 2000-06-17
PRIOR FILING DATE: 2000-06-17
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: TYO, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT PILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 7
LENGTH: 34
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                                                            DTLMISRIPEVI --- CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
   ----HCFPLPAMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.5%; Score 284; DB 4; Length 51
100.0%; Pred. No. 1.3e-25;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.1e-16;
hes 0;
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                                                                                                                            157 VITKTNDY-----CKSLPAALSATEIEKSIS 182
                                                                                                                                                                       :| |:|| |:|| 142 LTVLHQDWLNGKEYKCKVSNKALPA-PIEKTIS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 20.9%; Score 201; DB Best Local Similarity 100.0%; Pred. No. 3.1 Matches 34; Conservative 0; Mismatches
   DEIILPRGLEYTVEECTCEDCIKSKPKVDSD-
                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09854864
Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7, Application US/09854864
Patent No. 6774106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 100. Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Homo sapiens
US-09-854-864-7
                                                                                                                                                                                                                                                                                                                           US-09-854-864-6
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US-09-854-864-7
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88 EPKNTGSGLLGMANIDLEKSR------TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Mismatches 29; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.2%; Score 79.5; DB 2; Length 1009; Best Local Similarity 32.1%; Pred. No. 5; Matches 25; Conservative 9; Mismatches 29; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Sequence 1, Application US/08460626
| Patent No. 5837815
| GENERAL INFORMATION:
| APPLICANT: STWA LEV
| APPLICANT: STWA LEV
| TITLE OF INVENTION: PYK-2 RELATED PRODUCTS AND
| TITLE OF INVENTION: METHODS
| NUMBER OF SEQUENCES: 25
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Lyon & Lyon
| STREET: 633 West Fifth Street
| STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS S.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,626
FILING DATE: June 2, 1995
CLASSIFICATION: 435
PRIOR APPLICATION A435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/357,642
FILING DATE: December 15, 1994
ATTONNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 31/121
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READBLE FORM:
MEDIUM TYPE: S.5. Diskette, 1.44 Mb
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAK: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139 DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | | | :| :| 320
306 RSIRCLPL---EEGQAVL 320
                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                               US-08-357-642A-1
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US-08-460-626-1
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Patent No. 6774106

GENERAL INFORMATION:
APPLICANT: THELL, LARS EYDE
APPLICANT: THELL, LARS EYDE
APPLICANT: THELL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERBUCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR PLICATION NUMBER: US 60/204,039
PRIOR PLILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 60/214,591
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81 PKDTLMISRTPEVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 21;
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10.8%; Score 104; DB 4; I
Best Local Similarity 100.0%; Pred. No. 2.8e-05;
Matches 21; Conservative 0; Mismatches 0;
                                                                         155 ILVTTKTNDY-----CKSLPAALSATEIEKSIS 182
                                                                                                          Sequence 1, Application US/08357642A; Sequence 1, Application US/08357642A; Patent No. S837524; GENERAL INFORMATION: APPLICANT: Sinae Lev APPLICANT: Joseph Schlessinger TITLE OF INVENTION: PYKZ RELATED PRODUCTS; TITLE OF INVENTION: AND METHODS; NUMBER OF SEQUENCES: 16 CORRESPONDENCE ADDRESS: ADDRESSEE: Lyon & Lyon STREET: 633 West Pifth Street; STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 30071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,642A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 ILWTCLGLSLIISLAVFVLMF 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ILWTCLGLSLIISLAVFVLMF 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: December CLASSIFICATION: 536
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
US-09-854-864-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-357-642A-1
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US-09-854-864-8
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APPLICANT: DESM., JEBEN, GOEZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLBIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----KVD 139
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                            93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 78.5; DB 3;
19.9%; Pred. No. 1.1;
tive 35; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IEM PC compatible
COMPUTER: IEM PC COMPATIBLE
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
APPLICATION NUMBER: US/09/290,333
RILING DATE: 12-Apr-1999
CLASSIFICATION: vUMBON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                           140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                                                                                                                 210 QDH-----AMEAGSPVSTSPEPVETC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09290333 Patent No. 6316222 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                         108 ---RTGDEIILPRG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 19.99
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-290-333-2
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APPLICANT: Bram, Richard J.
APPLICANT: Bram, Richard J.
APPLICANT: VOI BULOW, GOLZ
TITLE OF INVENTION: A LYMPHOCYTE SUBFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                        'n.
                                                                                                                                                                                  88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                          249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLABFKQI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : : | : | | | : : | : | : : | 34 CPEEQYWDPLLGTCRSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57;
                                                                                                                                          15;
                                                                                             Length 1009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 293;
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                                                                                                                                        9; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 28-FEB-1997

CLASSIFICATION: 536

ATTONIEV/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REGISTRATION NUMBER: 27,742

REGISTRATION NUMBER: 1340-1-007

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

8.1%; Score 78.5; DB 2;
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches 73;
                                                                                                  DB 2;
                                                                                               Score 79.5;
Pred. No. 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08810572A
Patent No. 5969102
                                                                                                                                                                                                                                                                                                               306 RŚIRCLPL --- EEGOAVL 320
                                                                                                                                                                                                                                                                       139 DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAK: 201-343-100.
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
                                                                                             8.2%;
nilarity 32.1%;
Conservative 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO
                                 , MOLECULE TYPE: peptide US-08-460-626-1
                                                                                                                      1 Similarity
25; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
               linear
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               TOPOLOGY:
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                                                                                               Query Match
Best Local 6
                                                                                                                                            Matches
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------KVD 139
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---LEYTVEECTCEDCIKSKP----KVD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09848295
Patent No. 6623941
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Yu, Guo-Liang, et al.
TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 293;
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8.1%; Score 78.5; DE
Best Local Similarity 19.9%; Pred. No. 1.1;
Matches 41; Conservative 35; Mismatches
                                                                                                                                                                                                                                                                                                                                             TILLE DEFERENCE: PF25.PT

CURRENT APPLICATION NUMBER: US/09/879,919

CURRENT FILING DATE: 2001-06-14

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR PLILING DATE: 2001-05-25

PRIOR PLILNG DATE: 2001-05-25

PRIOR PLILNG DATE: 2001-05-25

PRIOR PLILNG DATE: 2001-03-23

PRIOR PLILNG DATE: 2001-03-23

PRIOR PLILNG DATE: 2001-03-16

PRIOR PLILNG DATE: 2001-03-16

PRIOR PLILNG DATE: 2000-12-13

PRIOR PLILNG DATE: 2000-12-13

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-10-23

PRIOR PLILNG DATE: 2000-0-12

PRIOR PLILNG DATE: 2000-0-12

PRIOR PLILNG DATE: 2000-0-12
                                                                                       140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                                210 QDH----AMEAGSPVSTSPEPVETC 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/016,812
PRIOR FILING DATE: 1996-03-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 22
                                                                                                                                                                                                                                          Sequence 22, Application US/09879919
Patent No. 6541224
  ---RTGDEIILPRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-09-879-919-22
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US-09-848-295-4
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                                                                                                                                                                                                                                                                                                   APPLICANT: Bram, Richard J.
APPLICANT: Bram, Rocks
von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
  --KVD 139
                         93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 CPEBQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI
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                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 8.1%; Score 78.5; D. Similarity 19.9%; Pred. No. 1.1; 41; Conservative 35; Mismatches
                                                                                       140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                  210 QDH-----AMEAGSPVSTSPEPVETC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
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;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2
                                                                                                                                                                                                                                          Sequence 2, Application US/09782857A Patent No. 6500428 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 293 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
108 ---RTGDEIILPRG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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Best Local Similarity
                                                                                                                                                                                                RESULT 17
US-09-782-857A-2
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152 GLKLSADQVALVYSTLGLCLCAVLCCFLVAVACFLKKRGDPCSCQP--RSRPRQSPAKSS 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 LEGRTAĞTDSANATNFIAFAAÇYNTSSLKSPITVQWFLEPNDTIRVVHNNQTVAFNTSDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/922,521
FILING DATE: 30-UUL-1992
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08179481

Patent No. 5624816

GENERAL INFORMATION:
APPLICANT: CARRAWAY, KERMIT L.
APPLICANT: FREGIEN, NEVIS L.
TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 MANIDLEKSRTGDEIILPRGLEYTVEECTCEDCI 132
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REGISTRATION NUMBER: 16,773
REFERNCE/DOCKET NUMBER: 200702/UM92-08CIP
TELECOMMINICATION INFORMATION:
TELECOMMINICATION 187000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%; Score 76; DB 1
Best Local Similarity 22.1%; Pred. No. 8.2;
Matches 34; Conservative 29; Mismatches
                                                                                                                      11 ODH----AMEAGSPVSTSPEPVETC 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1100 NEW YORK AVENUE, N.W
                                                                                140 SDHCFPLPAMEEGATILVTTKTNDYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-07-717-331F-2
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       셤
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Facent No. 6774106

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERENCE: A-668B
CURRENT FILING DATE: 2001-09-11
FILE REPERING DATE: 2000-05-12
FROM APPLICATION NUMBER: US 60/204,039
FRIOR PELING DATE: 2000-05-12
FRIOR APPLICATION NUMBER: US 60/214,591
FRIOR APPLICATION NUMBER: US 60/214,591
FRIOR APPLICATION NUMBER: 31
SOFTWARE: PATENT OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----KVD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---RIGDEIILPRG-----KVD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 I----SLAVFVLMFL-----LRKISSEPLKDEFKNTGSGLLGMANIDLEKS---- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93 CGQHPKQCAYFCENKLRSPVNLPPELRRQRSGEVENNSDNSGR-YQGLEHRGSEASPALP 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 CPEEQYWDPLLGTCWSCKTICNHQS-QRTCAFCRSLSCRKEQGKFYDHLLRDCISCASI 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%; Score 78.5; DB 4; Length 293; 19.9%; Pred. No. 1.1; tive 35; Mismatches 73; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 293;
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19.9%; Pred. No. 1.1;
tive 35; Mismatches
                                  FILE REFERENCE: PF527
CURRENT APPLICATION NUMBER: US/09/848,295
CURRENT FILING DATE: 2001-05-04
FRIOR APPLICATION NUMBER: 60/202,193
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
LENGTH: 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 SDHCFPLPAMEEGATILVTTKTNDYC 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108 ---RTGDEIILPRG-----
   TITLE OF INVENTION: Thereon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 41; Conservat
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Best Local Similarity
Matches 41; Conserva
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US-09-854-864-14
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREUMONIARE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SISFCVPQSDCARAKRAMEDEFYLELKEGLLEPLAIMERLAIISV---VGDGMRTLRGIS 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 CLGLSLI-----ISLAVFVLMFLLR-----KISSEPLKDEFKNTGSGLLGMANIDLE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 SNRLKNKIFIPVML-MAILALVLAQMIPEFSKIS----ISLAAL--FATISVLVITNSHP 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 TVEECTCE-DCIKSKPKVDSDHCF-----PLPAMEEGATILVTTKTNDYCKSLP--- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 KSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --KDE-----FKNTGSGLLGM----ANIDLEKSRTGDEIIL--PRGLEY 121
                                                                                                                                                                                                                                                                                                                                                 1 MTELAKOLLE-----LIYIVIGCOFLHTA-----YCSYKDKTNPVRLGTSA-FWT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                45 LLSITFIGGSYMPNMSIGIIVILLSLITLFKQVRİGTLPSLDEMK------ANI--E 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLQMAGQCSQNE------YFDSLLHACIP---CQL-'-----RCSSNTPPLT 36
                                                                                                                                                                                                                                                                                                   1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCN-ASVTNSVK-GTNAILWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 CORYCNASVTNSVKGTNAILWTCLGLSL----IISLAVFVLMFLLRKISSEPL----
                                                                                                                                                                                                                                                   49; Gaps
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                                                                                                                                                                                               Query Match 7.6%; Score 73.5; DB 4; Length 307; Best Local Similarity 26.2%; Pred. No. 4.5; Matches 48; Conservative 26; Mismatches 60; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.4%; Score 71.5; DB 4; Length 835; 21.0%; Pred. No. 32; tive 36; Mismatches 80; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----AALSATEI-----EKSIS 182
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Patent No. 6610836
GENERAL INFORMATION:
                                                                                                   ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 8740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 21.03
Matches 56; Conservative
  PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SEQ ID NO 2671
LENGTH: 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -09-489-039A-8740
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TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REPERENCE: PATHOG-07A
CURRENT APPLICATION NUMBER: US/09/583,110
FRIOR PELING DATE: US/09/583,110
FRIOR FILING DATE: US/09/583,111
FRIOR FILING DATE: US/09/583,131
FRIOR FILING DATE: 1998-06-30
FRIOR FILING DATE: 1998-05-12
FRIOR FILING DATE: US/09/583,131
FRIOR FILING DATE: US/09/583,131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCF----PLPAMEEGATILVTTKT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  880 CKKRCISD---CNCTAFANADIRNG--GSGCVIWTERLEDIRNYATDAIDGODLYVRLAA 434
GENERAL INFORMATION:

APPLICANT: June Nagrallah; Michael Nasrallah; and Joshua APPLICANT: Stein

TITLE OF INVENTION: A Receptor Protein Kinase Gene TITLE OF INVENTION: Encoded At The Self-Incompatability Locus UNDRER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.8%; Score 75; DB Best Local Similarity 17.6%; Pred. No. 13; Matches 33; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIPICATION: 800
ATTORNEY AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2671, Application US/09583110 Patent No. 6699703
                                                                                                                                                                             E: Yahwak & Associates
25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 857 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (203) 268-1951
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                                                                                                                                                                                                                                                   STATE: Connecticut COUNTRY: USA
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APPLICANT: Lynn Do
                                                                                                                                                                                                                           CITY: Trumbull
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-583-110-2671
                                                                                                                                                                                                                                                                                                   ZIP: 06611
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APPLICANT: THELLY, LARS EYDE
APPLICANT: THELLY, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
PRIOR PLILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SUCTION 10.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 CGQHPKQCAYFCENKLRSPVNLPP---ELRRQRSG-------EVENNSDNSGRYQGLE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66 I----SLAVFVIMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 LFHSSLSCOLIHQTCKRIADNDPNVS-YNLCVMSLESNPMSANASLEELGVIAVELALSN 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 LIHACIPCOL-----RCSSNTPPLTCORYCNASVTNSVKGTNAIL--WTCLGLSLIISL 68
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Sequence 11, Application US/09780717

Sequence 11, Application US/09780717

Sequence 11, Application US/09780717

APPLICANT: Bates, Nic

APPLICANT: Bates, Nic

APPLICANT: Allen, Stephen M.

TITLE OF INVENTION: No. 671366e1 Invertase Inhibitors and Methods

TITLE OF INVENTION: 6 Use

FILE REFERENCE: 035718/208677

CURRENT APPLICATION NUMBER: US/09/780,717

CURRENT FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: US 60/181,509

PRIOR APPLICATION NUMBER: US 60/181,509

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FREESEQ for Windows Version 4.0

LEMANT. 18 NO 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141 HRGSEAS-----PALPGLKLSADOVALVYSGGGGGDKTHTCPPCPAPE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 180;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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7.3%; Score 70.5; DE
Best Local Similarity 21.4%; Pred. No. 15;
Matches 36; Conservative 23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YTVEECTCEDCIKSKP--KVDSDH----
Sequence 18, Application US/09854864 Patent No. 6774106 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 36; Conserv
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US-09-780-717-11
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     Sequence 6022, Application US/09328352
Patent No. 6562968
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TILLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE: GTO99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Steve Daniel
APPLICANT: Steve Daniel
APPLICANT: James Gilmore
APPLICANT: James Gilmore
APPLICANT: James Gilmore
APPLICANT: Laura Stuve
TITLE OF INVENTION: DETECTION OF ALTERED EXPRESSION OF GENES REGULATING CELL
TITLE OF INVENTION: PROLIFERATION
FILE REPERENTE: PA-0003 US
CURRENT APPLICATION NUMBER: US/09/232,160
CURRENT PILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PERL Program
SEQ ID NO 18
LENGTH: 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 VTNSVKGTNAI-LWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANI- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 -DLEKSRTGDEIILPR-----GLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 YPDSLLHAC-IPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLG----LSLIIS 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 LAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEEC 126
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Best Local Similarity 24.7%; Pred. No. 9.9;
Matches 36; Conservative 29; Mismatches 67; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GDTVST-VNNHWKGLSNIQNSSNAEE 148
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Patent No. 6368794
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Acinetobacter baumannii
US-09-328-352-6022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: -
OTHER INFORMATION: 1299627
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US-09-232-160-18
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Sequence 6, Application US/08810572A

Sequence 6, Application US/08810572A

Patent No. 5969102

GENERAL INFORMATION:
APPLICANT: WICHARD

TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TITLE OF INVENTION: THEREOF

TOWNERS OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAMME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
TELEPHONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                  RESULT 31
US-08-810-572A-6
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Facent No. 6774106

GENERAL INFORMATION:
FAPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B

CURRENT PILING DATE: 2001-09-11

PRIOR PILICATION NUMBER: US 60/214,591

PRIOR PLICATION NUMBER: US 60/214,591

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-06-77

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 20

LENGTH: 59
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                                                                                                                                                                                                                      Sequence 44, Application US/09780717

Sequence 44, Application US/09780717

Patent No. 6713666

GENERAL INFORMATION:

APPLICANT: Helentjaris, Tim

APPLICANT: Helentjaris, Tim

APPLICANT: Allen, Stephen M.

TITLE OF INVENTION: of Use

TITLE OF INVENTION: of Use

FILE REFERENCE: 035718/208677

CURRENT APPLICATION NUMBER: US/09/780,717

CURRENT APPLICATION NUMBER: US 60/181,509

PRIOR PILING DATE: 2000-02-10

PRIOR FILING DATE: 2000-02-10

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 44
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                                                                                                     129 EDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKS---LPAALSAT 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 KPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
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Best Local Similarity 25.0%; Pred. No. 1.2;
Matches 15; Conservative 14; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 7.3%; Score 70; DB 4; Length 182
Best Local Similarity 24.8%; Pred. No. 5.4;
Matches 27; Conservative 23; Mismatches 51; Indels
ORGANISM: Homo sapiens
US-09-854-864-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Glycine max US-09-780-717-44
                                                                                                                                                                                      RESULT 29
US-09-780-717-44
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von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                         65
                                                                                                                                                            | ::|:| || |: || |: || CPEEQYMDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEGGKFYDHLLRDCISCASI 92
                                                                                                                         8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI
                                                            3,
Query Match 7.2%; Score 69.5; DB 2; Length 166; Best Local Similarity 25.0%; Pred. No. 5.4; Matches 15; Conservative 14; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09290333
Patent No. 6316222
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS:
```

8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65

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Gequence 15, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EXDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR PILING DATE: 2000-06-27

PRIOR PILING DATE: 2000-06-27

PRIOR PELING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1
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                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/810,572
FILING DATE: «Unknown»
ATTORNEY/AGRYT INFORMATION:
NAME: Jackson Esg., David A.
REGISTATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N.terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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US-09-252-991A-30641
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LENGTH: 166
TYPE: PRT
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APPLICANT: Bram, Richard J.
TITLE OF INVENTION: A LYMPHOCYTE SURPACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI 65
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MEDIUM TYPE: Floppy disk
COMPUTER: IBP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION DATE: 12-Apr-1999
CLASSIFICATION: «Unknown»
ATTORNEY AGENT INFORMATION: «Unknown»
ATTORNEY AGENT INFORMATION: "NAME: Jackson Esg., David A.
REGISSTRATION NUMBER: 26,742
REGISSTRATION NUMBER: 26,742
TELEPHONE: 201-487-5800
TELEPHONE: 201-487-5800
TELEPHONE: 201-491-1684
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Peb-2001
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SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/09782857A Patent No. 6500428 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N. terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 07601
COMPUTER READABLE FORM:
                                                                                                                                                      STATE: New Jersey
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                                                                                                                      CITY: Hackensack
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                                                                                 Floor
                                                                                                                                                                                               COUNTRY: USA
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US-09-782-857A-6
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Sequence 5429, Application US/09328352

Patent No. 6562958
GENERAL INFORMATION:
PAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBRICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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APPLICANT: STORMANN, THOMAS M.
APPLICANT: LEVINTHAL, CYNTHIA
APPLICANT: STORJOHANN, LANCR G.
APPLICANT: HAMMERLAND, LANCE G.
APPLICANT: RAAPCHO, KAREN J.
APPLICANT: RAAPCHO, KAREN J.
APPLICANT: NS PHARMACEVITCALS, INC.
TITLE OF INVENTION A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR FILE REFERENCE: 1094.2.
CURRENT APPLICATION NUMBER: US/09/695,481
CURRENT PILING DATE: 2000-10-24
PRIOR PLING DATE: 1999-10-25
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Best Local Similarity 24.6%; Pred. No. 65;
Matches 49; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , ORGANISM: Acinetobacter baumannii
US-09-328-352-5429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09695481
Patent No. 6534287
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US-09-695-481-2
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SOFTWARE: Patentin Ve
SEQ ID NO 2
LENGTH: 942
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LENGTH: 353
TYPE: PRT
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    TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FITLE REFERENCE: 107196.138
FILE REPERENCE: 107196.138
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .----A 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 SLA-VFVLMFLLRKISSEPLKDEFKNTGSGL-----LGMANIDL----EKSRTGDEII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 IPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKIS 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 SEPLKDEFKNTGS----GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCED 130
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7.2%; Score 69.5; DB 4; Length 217;
Best Local Similarity 25.7%; Pred. No. 8;
Matches 29; Conservative 11; Mismatches 46; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Reed, Randall
APPLICANT: Reed, Randall
APPLICANT: Reed, Randall
APPLICANT: Wau, King-Wai
APPLICANT: Yau, King-Wai
TITLE OF INVENTION: Oldactory Receptor Expession Libraries
TITLE OF INVENTION: Oldactory Receptor Expession Libraries
TITLE OF INVENTION: ad Methods of Making and Using Them
FILE REFERENCE: 001107.00105
CURRENT APPLICATION NUMBER: 05/09/465,901
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/112,605
PRIOR PILING DATE: 2001-12-17
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: PCR primer US-09-465-901-30
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ORGANISM: Mus musculus
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Best Local Similarity
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US-09-328-352-5429
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US-09-465-901-30
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LENGTH: 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77; Gaps
                                                                                                                                                                                                                         APPLICANT: LEVINTHAL, CYNTHIA
APPLICANT: STORJOHANN, LAURA
APPLICANT: HAMMERLAND, LANCE G.
APPLICANT: KRAPCHO, RAREN J.
APPLICANT: KRAPCHO, RAREN J.
APPLICANT: NES PHARNACEUTICALS, INC.
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence:Chimeric US-09-695-481-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.2%; Score 69.5; DB 4; Length 1043; Best Local Similarity 24.6%; Pred. No. 75; Matches 49; Conservative 21; Mismatches 52; Indels 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08660148
Patent No. 6211353
GENERAL INFORMATION:
APPLICANT: Burnett, J. P.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
APPLICANT: Sharp, Yoonne M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 --LLATLFVTVVFIIYRDTPVVKSSRELC----
                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 1094.2.6
CURRENT APPLICATION NUMBER: US/09/695,481
CURRENT FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: ,60/161,481
PRIOR FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 6
LENGTH: 1043
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163 -----DYCKSLPAALSA 174
                                      672 ILAGSKKKIĊTKKPRFMSA 690
                                                                                                                                          Sequence 6, Application US/09695481
Patent No. 6534287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 -----DYCKSLPAALSA 174
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                                                                                                                                                                                                      STORMANN, THOMAS M.
LEVINTHAL, CYNTHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Eli Lilly a
STREET: Lilly Corporat
CITY: Indianapolis
                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: STORMANN
APPLICANT: LEVINTHA
APPLICANT: STORJOHA
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COUNTRY: Unite
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62 LSLIISLAVFVLMFLLR-----KISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILP 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.2%; Score 69.5; DB
Best Local Similarity 24.6%; Pred. No. 90;
Matches 49; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591 --LLATLFVTVVFIIYRDTPVVKSSSRELC--
                                                                                                                                                                                      SOFTWARE: Patentin School of CURENT APPLICATION DATA:

APPLICATION NUMBER: US/08/660,148
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/282,853
FILING DATE:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GAYLO, PAUL J.
REFERENCE/DOCKET NUMBER: X-9419
TELECOMUNICATION INFORMATION:
TELECOMUNICATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   United States of America
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; Betent No. 6211353
; GENEAL INFORMATION:
    APPLICANT: Burnett, J. P.
    APPLICANT: Sharp, Robert L.
    APPLICANT: Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Eli Lilly and Company
STREET: Lilly Corporate Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163 -----DYCKSLPAALSA 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Lilly Corporter Indianapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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623 AGI-----CLGYLCTFCLIAKPK--QIYCYLQRIGIGLSPAMSYSALV---TKTNRIAR 671
                                                                                                                                                    117 RGLEYTVEEC---TCEDCIKSKPKVDSDHCF-----PLPAMEEGATILVTTKTN---- 162
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537 CKENEYVFDE--YTCKACQLG-SWPTDDLT---GCDLIPVQYLRWGDPEPIAAVVFACLG 590
                                                  62 LSLIISLAVFVLMFLLR-----KISSEPLKDEFKWTGSGLLGMANIDLEKSRTGDEIILP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   627 -----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLSLPLSISTAEVVSFH---- 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1706;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: HURD, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Pinger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        675 -KEKG--VYLSSKLKQLLQTQDKLTLPAGFSAAEIPK 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
7.2%; Score 69.5; DB 2;
Best Local Similarity 21.7%; Pred. No. 1.5e+02;
Matches 34; Conservative 22; Mismatches 44;
                                                                                       FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATE: 08/399,411
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      163 -----DYCKSLPAALSA 174
                                                                                                                                                                                                                                                                                                      672 ILAGSKKKIČTKKPRFMSA 690
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TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                623 AGI-----CLGYLCTFCLIAKPK--QIYCYLQRIGIGLSPAMSYSALV---TKTNRIAR 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CSQNEY-PDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTN----AILWTCLG 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: STORMANN, THOMAS M.
APPLICANT: STORMANN, THOMAS M.
APPLICANT: STORMANN, LANGA
APPLICANT: APMERLAND, LANGA
APPLICANT: HAMMERLAND, LANGE G.
APPLICANT: HAMMERLAND, LANGE G.
APPLICANT: NPS PHARMACEUTICALS, INC.
APPLICANT: NPS PHARMACEUTICALS, INC.
TITLE OF INVENTION: A NOVEL HUMAN METABOTROPIC GLUTAMATE RECEPTOR FILE REPERENCE: 1094-2.6
CURRENT APPLICATION NUMBER: US/09/695,481
CURRENT PELLING DATE: 2000-10-24
PRIOR FILING DATE: 1999-10-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.2%; Score 69.5; DB 4; Length 1212; Best Local Similarity 24.6%; Pred. No. 94; Matches 49; Conservative 21; Mismatches 52; Indels 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 1212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52; Indels
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Best Local Similarity 24.6%; Pred. No. 94;
Matches 49; Conservative 21; Mismatches
                                                                                                                                                                    NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REGISTRATION NUMBER: x-9419
TELECOMMUNICATION INFORMATION:
TELEPRAX: (317) 276-0756
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1212 amino acids
                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
US/08/660,148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 -----DYCKSLPAALSA 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-660-148-5
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-09-695-481-7
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TYPE: amino acid
TOPOLOGY: linear
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SOFTWARE: Patentin Ve
SEQ ID NO 7
LENGTH: 1212
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1706 amino acids
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STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-516-859A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       627 -----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLSLPLSISTAEVVSFH----- 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.2%; Score 69.5; DB 2; Length 1706; 21.7%; Pred. No. 1.5e+02; tive 22; Mismatches 44; Indels 57
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Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
Sequence 2, Application US/08399411
Patent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598 PVTVE----ITQNIKSTQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-LJ 1264
                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGIGTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPRAK: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                  STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                   92122
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CITY: Sa
STATE: C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-399-411-2
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94 SGLLGMANIDLEKSRIGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLP 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 PLICORYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----SVTDDLLKDSPSST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 7.2%; Score 69.5; DB 3; Best Local Similarity 21.7%; Pred. No. 1.5e+02; Matches 34; Conservative 22; Mismatches 44;
                                                                                                                                                                           FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPDELI, CALINTY A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 PVTVE-----ITQNIKSTQV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09586472; Patent No. 6323335
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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amino acid
FILING DATE:
ATTORNEY/AGENT II
NAME: Campbel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANT
                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                     US-09-528-706-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-125-028-2
                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 PVTVE-----ITQNIKSTQV--------SVTDDLLKDSPSST- 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 SGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCPPLP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 69.5; DB 3; Length 1706; Best Local Similarity 21.7%; Pred. No. 1.5e+02; Matches 34; Conservative 22; Mismatches 44; Indels 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Retinoblastoma Protein - Interacting TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS: ADDRESSE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                    FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
                                    APPLICATION NUMBER: US 09/528,706
                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-09-586-472-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 08/516,859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/528,706
                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
  <Unknown>
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1706 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09528706
Patent No. 6468985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Huang, Shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 47
US-09-528-706-2
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1279 NLIWQETGEEGFELYLDR-IDYQMSE-----KSLEKNRTNKLLEVAALAKVKTVRVTV 1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  105 ----EKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 SGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLP 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    627 -----NCESKKRRTASPPVLPKIKTETESDSTAPSCSLSLPLSISTAEVVSFH---- 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----SVTDDLLKDSPSST- 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 PLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: WADOUX, Isabelle
APPLICANT: WADOUX, Isabelle
APPLICANT: COLAVIZZA, Diddier
APPLICANT: LOIEZ, Annie
TITLE OF INVENTION: NOVEL COLD-SENSITIVE BREAD-MAKING YEASTS
FILE REFERENCE: levure sensible froid
CURRENT FILING DATE: 1998-007
EARLIER APPLICATION NUMBER: PCT/FR97/00254
EARLIER PILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 AMEEGATILVTTKTNDYCK----SLPAALSATEIEK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.2%; Score 69.5; DB 4; Best Local Similarity 21.7%; Pred. No. 1.5e+02; Matches 34; Conservative 22; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 69.5; DB 3;
24.8%; Pred. No. 2.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               598 PVTVE----ITQNIKSTQV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.2%; Score 69.5; D
Best Local Similarity 24.8%; Pred. No. 2.6e
Matches 34; Conservative 17; Mismatches
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 ISLAVFVLMFLLRKISSEPLKDE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , ORGANISM: Saccharomyes cerevisiae
US-09-125-028-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1331 NOKKNPDLSEDRPPALS 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --- KTNDYCKSLPAALS 173
                                                                                                                                                                                                                                                                     1706 amino acide
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 ISLAVFVLMFLLRKISSEPLKDE---------FKNTGSGLLGMANIDL---- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 ----EKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Sequence 2. Application US/08894344C

Batent No. 6172196

GENERAL INFORMATION:
APPLICANT: KANGAKI, Hideki
APPLICANT: TOKAI, Masaya
APPLICANT: TOKAI, Masaya
APPLICANT: OUGHI, Yasuhiro
APPLICANT: OUGHI, KOZO
TITLE OF INVENTION: DAW ENCODING PROTEIN COMPLEMENTING
TITLE OF INVENTION: LOW TEMPERATURE-SENSITIVE FERMENTABILITY
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FITZPATRICK, CELLA, HARPER & SCINTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.2%; Score 69.5; DB 3; Length 2958; 24.8%; Pred. No. 3.4e+02; tive 17; Mismatches 49; Indels 37.
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1440 Kb storage.
                                                                                                                                                                                                                                            MEDIUM TYPE: DIBRECL
COMPUTER: IBM PS/V
OPERATING SYTEM: MS-DOS Ver3.30
SOFTWARE: PATENT ALD Ver1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,344C
FILING DATE: 15-AUGUST-1997
RAPDICATION NUMBER: DESCEMBER-1996
APPLICATION NUMBER: PCT/JD96/03862
FILING DATE: 28-DECEMBER-1996
APPLICATION NUMBER: PCT/JD96/03862
FILING DATE: 27-DECEMBER-1996
ATTORNEY/AGENT INFORMATION:
NAME: PERTY, LAWIENCE S.
REGISTRATION NUMBER: 31865
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQUENCE CHARACTERISTICS:
LENGTH: 2958 amino acids
TELEGHT: 2958 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Saccharomyces cerevisiae
STRAIN: X2180-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1331 NOKKONPOLSEDRPPALS 1347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               160 --- KTNDYCKSLPAALS 173
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Best Local Similarity 24.8
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
US-08-894-344C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-894-344C-2
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US-08-579-940-7
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Sequence 7, Application US/08579940 Patent No. 5977315

Chatterjee, Malaya Kohler, Heinz

GENERAL INFORMATION: APPLICANT: Chatter APPLICANT: Kohler,

```
### PEPICANT: Chatterjee, Sunil K
TITLE OF INVENTION: MUTINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
TITLE OF INVENTION: MUTINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
TITLE OF INVENTION: MUTINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
TITLE OF INVENTION: MILE
CORRESPONDENCE ADDRESS:
STREET: 755 Page Mill Road
STATE: CA.
COUNTRY: USA
ZIP: 94304-1018
COMPUTER: Table Alto
STATE: Table Alto
STATE: Table Alto
COMPUTER: Table Compatible
COMPUTER: Table Alto
STATE: ```

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Run

Sequence:

Minimum DB Maximum DB

Database

Result Š.

Searched:

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Human BCM
Human B-C
Human BAF
Human BCM
Amino aci
Murine B
Mouse B C
Mouse B C
Muse B C
Human-mur
 Human-mur
A murine
A murine
Bub
Murine sub
Human TAC
 Protein o
Human pro
Human sub
Human nov
Human pol
Drosophil
Human 567
Human POL
Novel hum
Human POL
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Human POL
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Add11499
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Add1499
Add1499
Add1499
Add1999
AAE00507
ADG43717
ADG43717
ADG537060
AD153060
AAE058084
AAE15490
AAE15490
AAE15492
AAE15492
AAE15492
AAE15492
AAE15492
AAE15492
AAE15495
AAE15493
AAE15495
AAE15493
AAE15494
AAE15494
 AAU10949
AAW75783
 AAB36312
AAY94000
AAE09240
 AAY71914
AAO14130
ABB81488
 ABP60551
ABP97716
AAO29592
ADF72628
 ADK00765
AA014135
AAE35228
 AAE15498
AAO14136
 AAC14133
AAE35224
AAE35225
AAE35226
AAC14132
AAE35223
 61
61
61
 Aae15486 Human B-C
Aae15591 Human B-C
Aae15591 Human B-C
Aae15591 Human B-C
Aab08843 Amino aci
Aay9101 A human B-C
Aay1979 Human B-C
Aay01979 Human B-C
Aab06098 Human B-C
Aae00506 Human B-C
Aae00609 Human B-C
Aae01487 Human B-C
Aae35216 Human B-C
Aae36757 Human Lul
Adg43715 Human B-C
 Human B-c
Human B-c
Human BCM
Human Gen
Human tum
Amino aci
Human Ly1
Human B-C
Native hu
Human BCM
Human ECM
 ; Search time 36.3395 Seconds (without alignments) 335.635 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 Aae15488 B
Abg95060 B
Aab60699 B
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-10-077-137-1_COPY_8_41
201.
1 CSQNEYFDSLIHACIPCQLRCSSWTPPLITCQRYC 34
 Notal number of hits satisfying chosen parameters:
 2002273 segs, 358729299 residues
 SUMMARIES
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
 protein search, using sw model
 2005, 19:37:53
 AAE15486
ADA49366
AAE15485
AAE15501
AAE15484
AAB08843
AAY94001
AAE09241
 AAY71979
AAB60698
AAB60698
ABB81487
ABB81487
AAB28961
AAB285216
AAB4961
AAB60552
ABP97717
ABP67527
AAB67526
AAB67318
AAB67318
AAB67318
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Geneseq_23Sep04;*

geneseqp1980s;*

geneseqp200s;*

geneseqp2001s;*

geneseqp2001s;*

geneseqp2003s;*

geneseqp2003bs;*

geneseqp2003bs;*
 seq length: 0
seq length: 200000000
 В
 Length
 January 28,
 Query
Match
 Scoring table:
 Title:
Perfect score:
 22001
22001
22001
22001
22001
22001
22001
22001
```

Length 34;

```
Human, transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCWA; tumour necrosis factor; TNF; pymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; corbn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 Human B-cell maturation (BCMA) protein cysteine-rich consensus region.
Ade07852 Novel
 ALIGNMENTS
ADE07852
ADE08940
 AAE15486 standard; peptide; 34 AA
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567
7
 (first entry)
897
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
29.6
29.6
 Theill LE, Yu G;
 WO200187979-A2.
 Homo sapiens
 12-MAR-2002
59.5
59.5
 AAE15486;
 Ligand
 RESULT 1
 AAE15486
100
```

ಠ disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythemacosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein cysteine-rich consensus region The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand); having the consensus region of TACI, BCMA, or the TACI bCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, agastrointsethnal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic disease (asthma, hypersensitivity lung disconding the state of the state

Claim 1; Fig 10A; 94pp; English.

Sequence 34 AA;

```
The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &bgr; strands NO:2, bad E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antitheumatic, antinflammatory, antiartitic, dermatological, antidabetic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal. TC is useful for inhibiting TALL-1 dependent diabetes mellitus, multiple sclerosis, mysthaenia gravis, dependent diabetes mellitus, multiple sclerosis, mysthaenia gravis, crave's disease, autoimmune hemolytic anaemia, autoimmune thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococal glomerulonephritis and cute rheumatic fever, post-streptococal glomerulonephritis and polyarteritis nodosa. The present sequence represents a cysteine rich
 ö
 Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
 TALL-1; antagonist; immunosuppressive; antirheumatic; antiinflammatory; antiathritic; dermatological; antidiabetic; neuroprotective; antithyroid; antipyretic; nephrotropic; vacotropic; vacotne; autoimmune disease; rheumatorid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; Gododpasture's syndrome; pemphigus vulgaris; acute rheumatic fever; popt. Erreptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD;
 Gaps
 ö
 Indels
 ; Score 201; DB 5;
; Pred. No. 2.3e-18;
0; Mismatches 0;
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 Disclosure; Page 616; 618pp; English.
 domain (CRD) module of human BCMA.
 ADA49366 standard; peptide; 34 AA
 Human BCMA cysteine rich domain.
 Liu Y, Xu L;
 100.0%;
 14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
13-AUG-2002; 2002US-0403364P.
 24-OCT-2002; 2002WO-US034376.
 (first entry)
Query Match
Best Local Similarity 100.
Matches 34; Conservative
 cysteine rich domain
 WPI; 2003-403345/38.
 Shu H,
 WO2003035846-A2.
 Homo sapiens
 24-OCT-2001;
 20-NOV-2003
 01-MAY-2003
 ADA49366;
 Zhang G,
 ADA49366
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Gaps

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0

100.0%; Score 201; DB 6; 100.0%; Pred. No. 2.3e-18; ive 0; Mismatches 0;

34; Conservative

Matches

Similarity

Query Match Local

Sequence 34 AA;

SX

Length 34; Indels

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding patrner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; collitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 activator and intracellular cyclophilin ligand interactor, by
administering a binding partner for APRIL, a tumor necrosis factor family
 diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer
 transmembrane activator and intracellular CAML interactor; TACI;
 lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function
 Inhibiting activity of B cell maturation protein and/or transmembrane
 Human B-cell maturation (BCMA) protein extracellular domain.
CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 rheumatoid arthritis; atherosclerosis
 Claim 1; Fig 10A; 94pp; English.
 AAE15485 standard; peptide; 51
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-021459IP.
14-MAY-2001; 2001US-0021459I.
 14-MAY-2001; 2001WO-US015567
 (first entry)
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
 Yu G;
 WO200187979-A2
 Homo sapiens
 12-MAR-2002
 22-NOV-2001.
 rheill LE,
 AAE15485;
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 ligand
 RESULT 3
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell meturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/CCC BCMA in a mammal which is useful for treating B-cell or T-cell and/or BCMA in a mammal which is useful for treating B-cell or T-cell and/or BCMA in a mammal which is useful for treating B-cell or T-cell supphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatities, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (crohn's disease (multiple
 ö
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 Human; transmembrane activator and intracellular CAML interactor; TACI, cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; crobh's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
organs. The present sequence
 Gaps
 Human B cell maturation protein cysteine rich extracellular region.
 ö
 Length 51;
 Indels
 100.0%; Score 201; DB 5; 100.0%; Pred. No. 3.5e-18;
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
 CSONEYPDSLLHACIPCQLRCSSNTPPLTCQRYC 38
with leucocyte infiltration of the skin or is human BCMA protein extracellular domain
 0; Mismatches
 rheumatoid arthritis; atherosclerosis
 Disclosure, Fig 13; 94pp; English.
 Ź
 AAE15501 standard; peptide; 58
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567
 (first entry)
 Conservative
 WPI; 2002-066686/09.
 Local Similarity
 (AMGE-) AMGEN INC.
 Yu G;
 Sequence 51 AA;
 WO200187979-A2
 Homo sapiens
 34;
 12-MAR-2002
 22-NOV-2001
 rheill LE,
 AAE15501;
 Query Match
 ligand
 Matches
 AAE15501
 RESULT
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Matches
 AAB08843
 RESULT
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 The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNR family ligand), having the consensus region of TACI, BCMA, or the TACI/
 Human, transmembrane activator and intracellular CAML interactor, TACI, cytostatic, B cell maturation protein, BCMA, tumour necrosis factor; INF; Pyphoporoliferatined isorder; tumour; lung; gastrointestinal; pancreatic, procetate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; colons disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.
 /note= "Cysteine-rich consensus region; This is region is specifically claimed as SEQ ID NO: 7 in claim 1 of the specification"
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCWA cysteine-rich extracellular region
 Gaps
 ö
 5; Length 58;
 Indels
 ;
 100.0%; Score 201; DB 5
100.0%; Pred. No. 4e-18;
tive 0; Mismatches
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 /label= Transmembrane_domain
 Human B-cell maturation (BCMA) protein.
 Location/Qualifiers
 Disclosure; Fig 10A; 94pp; English.
 AAE15484 standard; protein; 181 AA
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-021459IP.
14-MAY-2001; 2001US-0021459I.
 14-MAY-2001; 2001WO-US015567.
 (first entry)
 Query Match
Best Local Similarity 100.'
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC
 Yu G;
 Sequence 58 AA;
 WO200187979-A2
 Homo sapiens
 12-MAR-2002
 22-NOV-2001
 Theill LE,
 AAE15484;
 ligand.
 Region
 Domain
 AAE15484
 RESULT
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 8888888
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ö
 The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a
BCWA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
 BCNA, necrosis factor-kB activator, NP-kB; gene expression; cancer, anti-cell death gene, apoptosis, viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
 Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
 ö
 Length 181;
 Indels
 57. .77
/note= "putative transmembrane domain"
 Score 201; DB 5;
Pred. No. 1.3e-17;
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 38
 0; Mismatches
 Location/Qualifiers
 AAB08843 standard; peptide; 184 AA
 Claim 32; Fig 7A; 53pp; English.
 99US-0121485P.
 100.0%;
 100.08;
 Amino acid sequence of human
 24-FEB-2000; 2000WO-US004925
 (first entry)
 (GEHO) GEN HOSPITAL CORP.
 Conservative
 is human BCMA protein
 WPI; 2000-558405/51.
 Query Match
Best Local Similarity
 Ting A;
 Sequence 181 AA;
 WO200050633-A1
 24-FEB-1999;
 Homo sapiens
 02-JAN-2001
 34;
 31-AUG-2000
 expression
 AAB08843;
 Seed B,
 Domain
```

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ö
 Human; BR41x2; TACI receptor; extracellular domain; BCWA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; stif4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; mysthemia gravis; multiple sclerosis; rheumatoid arthritis; asthms; bronchitis; emphysema; pyslonephritis; emphysema; pyslonephritis; ereal neoplasm; multiple myeloma; lymphoma; light chain neuropatritis; menene response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
 The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumnour necrosis factor (TNP) receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNP ligand. They may also be used
 Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 Gaps
 ö
 Length 184;
 Indels
 A human BCMA protein, a B cell protein related to TACI.
 100.0%; Score 201; DB 3; 100.0%; Pred. No. 1.3e-17;
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 0; Mismatches
 Disclosure; Page 152; 175pp; English.
 Yee DP;
 AAY94001 standard; protein; 184 AA
 07-JAN-2000; 2000WO-US000396.
 99US-00226533.
 Gross JA, Xu W, Madden K,
 (first entry)
 34; Conservative
 (ZYMO) ZYMOGENETICS INC
 WPI; 2000-452538/39.
N-PSDB; AAA58559.
 Local Similarity
 Sequence 184 AA;
 WO200040716-A2.
 20-OCT-2000
 07-JAN-1999;
 Homo sapiens
 13-JUL-2000.
 designing
 AAY94001;
 Query Match
 Matches
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c for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoinemune disease selected from systemic lupus erythematosus, myasthenia cyrolic moliple sclerosis and rheumatoid arthritis. The zinf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure, cylomerulonephritis, vasculitis, nephritis, pyelonephritis, renal coplasms, multiple myelomas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response immunosuppression, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, ioint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli
 ö
 The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TACI or ECMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or activity. TALL-1 and APRIL antagonists are used to block the interaction
 TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
 Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 Gaps
 Pitti RM;
 Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
 ö
 Length 184;
 Grewal I, Kim KJ, Marsters SA,
 Indels
 100.0%; Score 201; DB 3;
100.0%; Pred. No. 1.3e-17;
ive 0; Mismatches 0;
 8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 1 CSONEYPDSLLHACIPCOLRCSSNTPPLTCQRYC 34
 Ź
 Example 2; Fig 2; 160pp; English.
 AAE09241 standard; protein; 184
 16-FEB-2000; 2000US-0182938P.
22-AUG-2000; 2000US-0226986P.
 28-NOV-2000; 2000WO-US032378
 19-NOV-2001 (first entry)
 Query Match
Best Local Similarity 100.
Matches 34; Conservative
 Ashkenazi AJ, Dodge KH,
 (GETH) GENENTECH INC.
 WPI; 2001-541628/60.
N-PSDB; AAD15902.
 Human BCMA protein.
 Sequence 184 AA;
 WO200160397-A1.
 Homo sapiens.
 23-AUG-2001.
 antagonists
 AAE09241;
 Yan M;
 RESULT 8
 AAE09241
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ö
 The present invention relates to Tumour necrosis factor (TNF) and Apolrelated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for requlating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rheumatoid arthritis, systemic lupus
 Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
between APRIL and TALL-1 with TACI or BCMA. They are useful for treating
 a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The present sequence is human BCMA protein
 Gaps
 Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
 .
0
 Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 Length 184;
 Indels
 100.0%; Score 201; DB 4;
100.0%; Pred. No. 1.3e-17;
tive 0; Mismatches 0;
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 Human B cell maturation factor (BCMA) protein.

 .62
 /label= Extracellular_domain

 Claim 37; Page 104-105; 112pp; English.
 (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 Location/Qualifiers
 AAY71979 standard; protein; 184 AA
 01-MAY-2000; 2000US-0201012P.
 05-MAY-2000; 2000WO-US012266
 99US-0132892P
 (first entry)
 34; Conservative
 WPI; 2001-016094/02.
 Local Similarity
 N-PSDB; AAD02125.
 Sequence 184 AA;
 WO200068378-A1.
 Homo sapiens
 06-MAY-1999;
 28-MAR-2001
 16-NOV-2000
 AAY71979;
 8
 Query Match
 Domain
 Shu HS
 Matches
 RESULT 9
 AAY71979
 858885588
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erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rhematic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a human B cell maturation factor (BCMA) protein. It is the receptor for TALL-1 protein. Drotain. BCMA gene is located on chromosome by brain, muscle, heart, lung, kidney, pancreas, testis and placenta. BCMA is absent in the pro-B lymphocyte stage but its expression increases with B lymphocyte maturation
 ö
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; b-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; uccil carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour.
 The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the
 Gaps
 .
 Length 184;
 Schneider P;
 Indels
 100.0%; Score 201; DB 4; 100.0%; Pred. No. 1.3e-17;
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 Tschopp J,
 1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
 0; Mismatches
 AAB60698 standard; protein; 184 AA.
 Browning J, Ambrose C,
 Claim 20; Fig 1; 59pp; English.
 Human BAFF receptor (BAFF-R).
 16-AUG-2000; 2000WO-US022507.
 17-AUG-1999; 99US-0149378P.
11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
 (first entry)
 Local Similarity 100.
1es 34; Conservative
 (APOT-) APOTECH R & D SA.
 WPI; 2001-202866/20.
 (BIOJ) BIOGEN INC
 Sequence 184 AA;
 N-PSDB; AAF59998
 WO200112812-A2.
 Homo sapiens.
 22-MAY-2001
 22-FEB-2001
 Thompson J;
 Mackay F.
 AAB60698;
 Query Match
 Best Loca
Matches
 AAB60698
ID AAB6
 RESULT
 88888888888888888888
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treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R.

"Specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, grave's disease, multiple myeloma, B-cell carcinomas, lumphomas, lumphoma
 ö
 Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 gene therapy, cancer, nephrotropic; renal disorder, autoimmine disease, carcinoma, lung, colon, breast, prostate, Grave's disease, hypertension, systemic lupus erythematosus; SLE, inflammation, cardiovascular disease,
 B-cell lympho-proliferative disorder, BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCMA; B cell maturation protein.
 Gaps
 Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 ö
 Rennert P;
 100.0%; Score 201; DB 4; Length 184; 100.0%; Pred. No. 1.3e-17;
 Indels
 Cachero T, Ambrose C,
 ö
 1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 0; Mismatches
 present sequence represents human BAFF-R
 cell maturation protein (BCMA).
 AAE00506 standard; protein; 184 AA
 05-OCT-2000; 2000WO-US027579.
 99US-0157933P.
 11-FEB-2000; 2000US-0181807P.
 Thompson J,
 (first entry)
 34; Conservative
 (BIOJ) BIOGEN INC. (APOT-) APOTECH R & D SA.
 WPI; 2001-266242/27
 Best Local Similarity
 N-PSDB; AAD03844.
 Sequence 184 AA;
 WO200124811-A1
 06-OCT-1999;
 Schneider P,
 31-JUL-2001
 Homo sapiens
 12-APR-2001
 AAE00506;
 Query Match
 Human B
 Matches
 8
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The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation Inducing Ligand Receptor (ARRIL-R) also referred as B cell maturation protein (BRM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinoma, breast carcinoma, breast carcinoma, prostate carcinoma, and other carcinoma, breast carcinoma, breast carcinoma, prostate carcinoma, and other carcinoma whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's diseases, renal disorders, B-cell lympho-proliferative disorders, immunosuppressive diseases, organ transplantation, inflammation and human immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is human APRIL-R also referred as BCMA or BCM protein
 ö
 Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antidiabetic; nephrotropic; hypotensive; qene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthemia gravis; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; renal neoplasm; multiple myeloma; amyloidosis; nenal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft rejection; Crohn's disease.
 Gaps
 ö
 Score 201; DB 4; Length 184;
Pred. No. 1.3e-17;
 Indels
 Human BCMA receptor related protein SEQ ID NO:7.
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 8 CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 0; Mismatches
 Grant FJ;
 ABB81487 standard; protein; 184 AA
 Claim 3; Fig 3A; 85pp; English.
 100.0%;
 100.04;
 20-DEC-2000; 2000US-0257131P.
28-JUN-2001; 2001US-0301715P.
29-AUG-2001; 2001US-0315565P.
 05-NOV-2001; 2001WO-US047018
 07-NOV-2000; 2000US-0246449P
 Gross JA, Xu W, Henne RM,
 Best Local Similarity 100.0
Matches 34; Conservative
 02-SEP-2002 (first entry)
 (ZYMO) ZYMOGENETICS INC.
 WPI; 2002-508212/54.
 Sequence 184 AA;
 WO200238766-A2.
 Ното варіелв.
 16-MAY-2002
antagonist.
 ABB81487;
 Query Match
 RESULT 12
 ABB81487
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The present invention describes a nummin tension includes account tecepool designated Ziffil2 (I). (I) has cytostatic, immunosuppressive, dermatological, antiafilammatory, neuroprotective, antidiabetic, antiathmatic, mephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Zinfil2 (e.g. ZINFA), for treating disorders and diseases associated with B complexity in a mammal, the activity of a ligand that binds Zinfil2 (e.g. ZINFA), for treating disorders and diseases associated with B complexity in a mammal, the proliferation of tuneur calls. (I) is useful for treating autoimmune disorders such as systemic lupus erythematosus, myasthenia continumed arbititis, bronchitis, emphysema and end stage renal failure cor renal disease such as glomerulomophritis, vasculitis, chronic lymphoid cor renal disease such as glomerulomophritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft rejection and Crohn's disease. (I) is useful for codulating the immune system. for regulating B cell responses and development, for modulating development of other cells, antibody communication. The presents expresents a protein which is given in the presents appresents a protein which is given in the presents.
 ö
 isolated human tumor necrosis factor receptor polypeptide, termed 12, useful for treating autoimmune disorders, emphysema, end stage failure or renal disease and lymphoma.
 present invention describes a human tumour necrosis factor receptor
 Gaps
 Colorectal cancer; metastasis; differential expression; cytostatic;
 ö
 Length 184;
 Indels
 Metastatic colorectal cancer-associated polypeptide.
 0
 100.0%; Score 201; DB 5; 100.0%; Pred. No. 1.3e-17
 in the exemplification of the present invention
 34
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC
 0; Mismatches
 Disclosure; Page 135-136; 154pp; English.
 ABP54694 standard; protein; 184 AA.
 (EOSB-) BOS BIOTECHNOLOGY INC. (UYCA-) UNIV CASE WESTERN RESERVE.
 diagnosis; gene therapy; vaccine.
 27-FEB-2001; 2001US-0272206P.
02-APR-2001; 2001US-0281149P.
17-APR-2001; 2001US-0284555P.
 27-FEB-2002; 2002WO-US006001
 (first entry)
 34; Conservative
 Mack DH, Markowitz SD;
 WPI; 2002-698677/75.
N-PSDB; ABQ81560.
 Similarity
 Sequence 184 AA;
 WO200268677-A2.
 Homo sapiens
 30-DEC-2002
 06-SEP-2002.
 ABP54694;
 Query Match
Best Local S
 Novel
Ztnfr
 renal
 RESULT 13
ABP54694
 Matches
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The present sequence is the protein sequence of a human polypeptide encoded by a gene that exhibits decreased expression in colon cancerderived metastases compared to normal colon tissue. It is an example of claimed polypeptides that are encoded by genes which are differentially expressed in metastatic colorectal cancer cells. Such polypeptides are useful in diagnostic and prognostic assays, for raising antibodies useful e.g. in immunotherapy, and in screening for modulator compounds of therapeutic value
 cancer, useful for
 New genes that are up- or down-regulated in colorectal cancer, useful for diagnosing colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating
 Human; tumour; B-cell maturation antigen; transmembrane activator; calcium-modulator; cyclophilin ligand-interactor; TAC1; gene therapy; neoplasm; chronic lymphocytic leukaemia; lymphoproliferative disease; non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma.
 Gaps
 B-cell maturation antigen and transmembrane activator and calcium-modulator and cyclophilin ligand-interactor, useful for treating disorders e.g. inflammation or lymphoma.
 ö
 Length 184;
 Indels
 ..
0
 ; Score 201; DB 5;
; Pred. No. 1.3e-17;
0; Mismatches 0;
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 41
 8. .41
/note= "Cysteine rich region"
 "Extracellular domain"
 "Antigenic epitope"
 Human B-cell maturation antigen (BCMA).
 Location/Qualifiers
 Ä
 Claim 8; Page 255; 260pp; English
 AAE28961 standard; protein; 184
 100.0%;
 20-FEB-2001; 2001US-0270274P.
12-APR-2001; 2001US-0283447P.
 06-FEB-2002; 2002WO-US003500
 27-JAN-2003 (first entry)
 34; Conservative
 ZYMO) ZYMOGENETICS INC.
 ...54
/note=
 1. .48
/note=
 BCMA; multiple myeloma
 WPI; 2002-723183/78.
N-PSDB; AAD46410.
 Query Match
Best Local Similarity
 colorectal cancer.
 Sequence 184 AA;
 WO200266516-A2.
 Kindsvogel W;
 Homo sapiens
 29-AUG-2002
 AAE28961;
 Region
 Domain
 Region
 Matches
 RESULT 14
 Key
 AAE28961
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The invention relates to the manufacture of a composition for inhibiting the proliferation of tumour cells. The method involves using an antibody component that binds both the B-cell maturation antigen (BCMA) and the transmembrane activator and calcium-modulator and cyclophilin ligand-interactor (TACI). BCMA and TACI binding antibody compositions are useful for inhibiting proliferation of tumour cells, particularly inhibiting proliferation of tumour cells, particularly inhibiting production or a disorder consisting of neoplasm, chronic lymphocytic leukaemia, multiple myelloma, non-Hodgkin's lymphoproliferative disease or light chain gammopathy or inflammation lymphoptoliferative disease or light chain gammopathy or inflammation e.g. asthma. The invention is also useful in gene therapy. The present is
 Disclosure; Page 63; 67pp; English.
 human BCMA protein
XXXCCCCCCCCCXXX
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Sequence 184 AA;

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ö
 Length 184;
 Indels
 ö
100.0%; Score 201; DB 5;
100.0%; Pred. No. 1.3e-17;
iive 0; Mismatches 0;
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 Best Local Similarity 100.
Matches 34; Conservative
 Query Match
 Š
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AAE35216 standard; protein; 184 AA RESULT 15 AAE35216 

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AAE35216;

Human B-cell maturation receptor (BCMA) protein.

(first entry)

28-MAY-2003

Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis, asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; B-cell maturation receptor; BCMA; receptor.

Homo sapiens

WO200294852-A2

28-NOV-2002

20-MAY-2002; 2002WO-US015910.

24-MAY-2001; 2001US-0293343P.

(ZYMO ) ZYMOGENETICS INC

Gross JA; Rixon MW,

WPI; 2003-148455/14.

N-PSDB; AAD53754.

ö Transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI)-immunoglobulin fusion protein, for treating cancer o diabetes, comprises a TACI receptor group and an immunoglobulin group.

Disclosure; Col 100; 71pp; English.

The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTMF)2 or ZTNF4; and an immunoglobulin group comprising a constant region of an

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ö
immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and astima, renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in (BCMA) protein used in the invention
 The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &bgr; strands D and B that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has
 Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
 human; TALL-1; antagonist; immunosuppressive; antirheumatic; antifilammatory; antiarthritic; dermatological; antidiabetic; neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatodia arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple soleroals; myasthaenia gravis; Grave's disease; autoimmune chemolytic anaemia; autoimmune thrombocytopenic purpura; Goodpasture s syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA.
 Gaps
 ö
 Length 184;
 Indels
 100.0%; Score 201; DB 6; 100.0%; Pred. No. 1.3e-17;
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 ; Pred. No. 1.3
0; Mismatches
 (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 Claim 62; Page 613; 618pp; English.
 ADA49361 standard; protein; 184 AA
 Zhang G, Shu H, Liu Y, Xu L;
 24-OCT-2001; 2001US-0345106P.
14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
 13-AUG-2002; 2002US-0403364P
 24-OCT-2002; 2002WO-US034376
 20-NOV-2003 (first entry)
 34; Conservative
 WPI; 2003-403345/38.
N-PSDB; ADA49360.
 Human BCMA protein.
 Local Similarity
 Sequence 184 AA;
 WO2003035846-A2
 Homo sapiens.
 01-MAY-2003
 antagonist.
 ADA49361;
 Query Match
 Best Loc
Matches
 RESULT 16
 ADA49361
 8888888888888
 셤
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The present invention relates to the use of an agonist or antagonist of Genoxit activity for preventing or treating obesity. Genoxit is a member of the Tumour Necrosis Factor Receptor Super Family and is a Type III transmembrane protein. The agonists or antagonists of the invention are useful for treating or preventing obesity-related diseases or disorders, e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease, heart disease (e.g. cardiac insufficiency, coronary insufficiency, high blood pressure), hypertension, stroke, syndrome X, diabetes mellitus (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic complications, e.g. microangiopathic lesions, ocular lesions,

8866666666666888

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Gaps

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Length 184; Indels

100.0%; Score 201; DB 6; 100.0%; Pred. No. 1.3e-17; iive 0; Mismatches 0;

Ouery Match Best Local Similarity 100. Matches 34; Conservative

Sequence 184 AA;

retinopathy, neuropathy and renal lesions

1 CSONEYPDSLIHACIPCOLRCSSNTPPLTCQRYC 34

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ö
 dermatological, antidiabetic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal is useful for treating autoimmune diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, crave's disease, autoimmune hemolytic anaemia, autoimmune thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis and polyarteritis nodosa. The present sequence represents human BCMA.
 Human, genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant; antidiabetic; hypotensive; ophthalmological; neuroprotective; nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family; Type III transmembrane protein; insulin resistance; atherosclerosis; atheromatous disease; heart disease; hypertension; stroke; syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia.
 Gaps
immunosuppressive, antirheumatic, antiinflammatory, antiarthritic,
 ;
0
 100.0%; Score 201; DB 6; Length 184; 100.0%; Pred. No. 1.3e-17;
 Indels
 ;
0
 1 CSQNEYFDSLLHACIPCOLRCSSNTPPLICORYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 l. .54
/label= Extracellular domain
 /label= Gln, Lys
55. .77
/label= Transmembrane_domain
 /label= Intracellular_domain
 0; Mismatches
 Location/Qualifiers
 ABR40082 standard; protein; 184 AA
 (first entry)
 Best Local Similarity 100.
Matches 34; Conservative
 .184
 Sequence 184 AA;
 Misc-difference
 WO2003013582-A1
 Human Genoxit
 Homo sapiens
 27-JUN-2003
 20-FEB-2003
 Query Match
 ABR40082;
 Domain
 Domain
 Domain
 RESULT 17
 Key
 ABR40082
 8X8888888888X8
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The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNT-delta/APRIL). The antibody of the invention has dermatological, immunosupressive, antianflammatory, antirheumic, antiarrhritic, cytostatic, antianaemic, antiallergic, antiabetic, neuroprotective, ophthalmological, tuberculoscalic, antiabetic, antipsoriatic, anti-HIV, antiatheric, assobropic, thyromimetic, and haemostatic activity. The antibody or its fragment are useful for treating, preventing or
 APRIL; scFv; immunospecific; tumour necrosis factor delta; TNP-delta; dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; cytostatic; antianaemic; antiallergic; antiathmatic; neuroprotective; ophthalmological; tuberculostatic; antidiabetic; antipsoriatic; anti-HIV; antiarteriosclerotic; vasotropic; thyromimetic; antibaconiatic; anti-FIV; antiarteriosclerotic; vasotropic; thyromimetic; inflammatory disorder; prolliferative disorder; single chain antibody; antibody; human; BCMA; tumour necrosis factor.
 Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 Disclosure; Page 222; 225pp; English.
 Ž
 Human tumour necrosis factor BCMA.
 ABP60552 standard; protein; 184
 22-MAY-2002; 2002WO-US016106.
 24-MAY-2001; 2001US-0293100P.
 (HUMA-) HUMAN GENOME SCI INC.
 28-MAR-2003 (first entry)
 WPI; 2003-156740/15.
 WO200294192-A2
 Homo sapiens,
 28-NOV-2002.
 ABP60552;
 syndrome.
 Ruben SM;
 18
 g
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New use of agonist or antagonist of Genoxit activity for preventing or treating obesity-related diseases or disorders, e.g. hyperlipidemia and atherosclerosis.

Briggs K;

Lucas J, Dialynas D, WPI; 2003-268160/26. N-PSDB; ACC00340.

(GEST ) GENSET SA.

05-AUG-2002; 2002WO-IB003498. 06-AUG-2001; 2001US-0310754P. Disclosure, Page 32; 35pp; English

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human, disease or disorder such as autoimmune disease, marging, most disease (GVHD). The autoimmune disease is systemic lupus not disease (GVHD). The autoimmune disease is systemic lupus erythematosus, rheumatoid arthritis or Sjogram's syndrome. The antibody is useful for detecting, diagnosing, prognosing, treating, preventing or ameliorating a disease or disorder associated with aberrant APRIL or APPRIL ameliorating cancer such as Non-Hodgkin's lymphoma or multiple myeloma in
 The present sequence represents a human BCMA polypeptide. The specification also describes TACI and BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April bind to the TACI receptor, while TNF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for preparing a composition for treating systemic lupus erythematosus
 Human, TACI, BR3; receptor; tumour necrosis factor ligand; TNF ligand;
TALL-1; April; systemic lupus erythematosus; BCMA.
 Gaps
 New nucleic acid encoding a TACIs or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus
 ö
 Length 184;
 Indels
 ö
 100.0%; Score 201; DB 6; 100.0%; Pred. No. 1.3e-17;
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 0; Mismatches
 Amino acid sequence of human BCMA receptor.
 Σ
 Yan
 ABP97717 standard; protein; 184 AA
 Disclosure, Fig 2; 153pp; English.
 Ridgway J,
 03-AUG-2001; 2001US-0310114P.
30-APR-2002; 2002US-0377171P.
 24-JUL-2002; 2002WO-US023487
 (first entry)
 34; Conservative
 (GETH) GENENTECH INC
 Dixit V, Grewal I,
 WPI; 2003-256560/25.
N-PSDB; ABZ68871.
 Similarity
 Sequence 184 AA;
 WO2003014294-A2.
 Homo sapiens
 28-MAY-2003
 20-FEB-2003.
 ABP97717;
 Query Match
Best Local S
 Best Loc
Matches
 RESULT 19
 요
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Sequence 184 AA;

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 the manufacture of a medicament, particularly as active ingredients in a composition for treating cancer, e.g. multiple myeloma cell, chronic lymphocytic leukaemia, B cell leukaemias, or lymphomas in humans, sheep, primates, goats, bovines, equines, porcines, lupines, canines or felines. The polymucleotide (I) or polypeptide can be used for screening anti-cancer agents, and generating antibodies or immunoconjugates for treating or preventing the above-mentioned diseases. The polymucleotide,
 encoded
 The present invention describes an isolated polynucleotide (I), which is overaxpressed in haematological malignancies, and which encodes a polypeptide or an immunogenic fragment of the polypeptide. Also described: (I) an isolated polypeptide; (2) an expression vector comprising (I) operably linked to an expression control sequence; (3) a host cell comprising an expression vector; (4) an isolated antibody that specifically binds to the polypeptide or its immunogenic fragment; and (5) immunoconjugates comprising the antibody above, or an antibody that specifically binds to a polypeptide, or its immunogenic fragment, encoded by (1). (I) has cytostatic and immunostimulant activities, and can be used in vaccines and immunotherapy. The immunoconjugates are useful in
 polypeptide or antibody can be used for detecting, diagnosing or prognosticating the haematological malignancies described above. The present sequence is used in the exemplification of the present invention.
 haematological malignancy; immunoconjugate; cytostatic; immunostimulant; vaccine; immunotherapy; cancer; multiple myeloma cell; chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
 New hematological malignancy-related genes and polypeptides, useful for screening anti-cancer agents, and generating antibodies or immunoconjugates for treating e.g. multiple myeloma cell or chronic
 Gaps
 Ordonez N;
 ö
 Length 184;
 Indels
 Wang A,
 ; Score 201; DB 6;
; Pred. No. 1.3e-17;
0; Mismatches 0;
 Clapper JD,
 34
 CSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
 Claim 9; SEQ ID NO 4; 307pp; English.
 Ź
 Human Ly1732P protein SEQ ID NO:4.
 Mannion J,
 ADD67527 standard; protein; 184
 100.0%;
llarity 100.0%;
Conservative 0;
 22-JAN-2003; 2003WO-US002353
 22-JAN-2002; 2002US-00057475
 Algate PA,
Mcneill PD;
 lymphocytic leukemia.
 WPI; 2003-598749/56.
 (first
 (CORI-) CORIXA CORP
Query Match
Best Local Similarity
Matches 34; Conser
 N-PSDB; ADD67526
 Sequence 184 AA;
 WO2003062401-A2
 Homo sapiens.
 15-JAN-2004
 31-JUL-2003
 Gaiger A,
Carter L,
 ADD67527;
 RESULT 20
 셤
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The present invention relates to an isolated monoclonal antibody which binds to a transmembrane activator of and CAML interactor (TACI) receptor. The TACI antibodies are useful for medulating TALL-1 or TACI polypeptide biological activity in mammalian cells, or for diagnosing and treating pathological conditions associated with TNF and TNF receptor-related molecules, e.g. cancer or immune-related disease, such as systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome, systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome, systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome, glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or infectious diseases including AIDS, hepatitis infection, bacterial infection, fungal infection, rottozoal infection and parasitic infection. The present sequence represents native human BCMA.
 New anti-TACI receptor monoclonal antibody, useful for diagnosing and treating pathological conditions associated with tumor necrosis factor, e.g. cancer or immune-related disease, such as rheumatoid arthritis or
 CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;
Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
 Antibacterial; antiparasitic; systemic lupus erythematosus; diabetes mellitus; AIDS; BCMA.
 Disclosure, SEQ ID NO 6; 110pp; English.
 Kim KJ,
 25-JUL-2003; 2003WO-US023421.
 25-JUL-2002; 2002US-0398530P
 Grewal I,
 (first entry)
 34; Conservative
 (GETH) GENENTECH INC.
 WPI; 2004-143841/14.
N-PSDB; ADK00755.
 Local Similarity
 Native human BCMA.
 Chuntharapai A,
 Sequence 184 AA;
 WO2004011611-A2
 Homo sapiens.
 06-MAY-2004
 05-FEB-2004.
 12-MAR-2002
 psoriasis.
 ADK00756;
 æ
 AAE15488;
 Query Match
 Best Loc
Matches
 RESULT 23
 AAE15488
 à
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 immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCWA), or an antibody against BCWA or a BCWA ligand (the mammal has or is at risk of developing multiple sclerosis). The method of the invention has neuroprotective, nootropic, and antiinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence represents human BCMA.
 The invention relates to a novel method for treating a neurodegenerative
 human; neurodegenerative immunological disorder; demyelination;
Central Nervous System; CNS; inflammation; B-cell maturation antigen;
BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
 Treating a neurodegenerative immunological disorder, e.g. demyelination
 or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
 Gaps
 Gaps
 ö
 .
0
 Length 184;
 Length 184;
 Indels
 Indels
 Score 201; DB 7;
Pred. No. 1.3e-17;
Mismatches 0;
 100.0%; Score 201; DB 7;
100.0%; Pred. No. 1.3e-17;
iive 0; Mismatches 0;
 1 CSQNEYFDSLIHACIPCOLRCSSNTPPLICQRYC 34
 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 41
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 Human B-cell maturation antigen SEQ ID NO:1.
 ADG43715 standard; protein; 184 AA
 Claim 8; Page 68-69; 72pp; English.
 ch
1 Similarity 100.0%; P:
34; Conservative 0;
 21-FEB-2003; 2003WO-US005147.
 21-FEB-2002; 2002US-0358427P.
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 34; Conservative
 WPI; 2003-721758/68.
Query Match
Best Local Similarity
 Kalled SL, Reid H;
 (BIOJ) BIOGEN INC.
 N-PSDB; ADG43716.
 Sequence 184 AA;
 WO2003072713-A2.
 Homo sapiens.
 gene therapy
 26-FEB-2004
 04-SEP-2003
 ADG43715;
 Matches
 RESULT 21
 RESULT 22
 ADK00756
ID ADK0
XX
 ADG43715
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Yan M;

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 Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;
 Gaps
 .
0
 Indels
 Human BCMA-immunoglobulin Fc region fusion protein.
100.0%; Score 201; DB 8;
100.0%; Pred. No. 1.3e-17;
ive 0; Mismatches 0;
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 AAE15488 standard; protein; 283 AA
 MAKEX EXEX S
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ADK00756 standard; protein; 184 AA

protein 90;

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ö
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein.
 diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermaritis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, infilammatory bowel disease (Crohn's disease, colltis), acleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atheroscies, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein
 The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering specific binding partner for ARRIL (970, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function
 Gaps
 ö
 Length 283;
 Indels
 , 2e-17;
0;
 DB 5;
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 38
 Human translocation (4; 16)(q26; p13) protein.
 ; Pred. No. 2e-
0; Mismatches
 100.0%; Score 201; 100.0%; Pred. No. 2
 Disclosure, Fig 10B; 94pp; English
 ABG95060 standard; protein; 288
 14-MAY-2001; 2001WO-US015567.
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 34; Conservative
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
 Theill LE, Yu G;
 Sequence 283 AA;
 WO200187979-A2
 Homo sapiens.
 04-DEC-2002
 22-NOV-2001.
 ABG95060;
 ligand
 RESULT 24
 ABG95060
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Chromosome aberration; oncogenic fusion protein; cancer;

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The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion corrected with chromosomal aberrations yielding oncogenic fusion collina (1). treating ancerous cells containing (1) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein containing Hasp90-inhibitor. The method is useful for treating administering HSP90-inhibitor. The method is useful for treating concepanic fusion protein, treating cancerous cells containing fusion protein protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein is oform dependent on heat shock protein (HSP)-90 (e.g. protein isoform in patient heterozygous for (II). The method is useful containing disease e.g. hemmatopoietic disorder such as T or B cell (IV) methoms, chronic myeloid leukaemia (CML), APL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid containing states and processing mutant processing method is carcinoma, Baking's sarcoma, melanoma, Inposarcoma and
 ö
 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90.
 synovial sarcoma. The method is also useful for treating viral infections. This represents a protein encoded by the DNA sequence of a
proliferative disease; cellular protein isoform; heat shock protein 90 HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder; T cell lymphona; B cell lymphoma; chronic myeloid leukaemia; CML; acute myeloid leukaemia; AML; ofronic myelomoncytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour; papillary thyroid carcinoma; Ewing's sarroma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
 Gaps
 ô
 Length 288;
 Indels
 100.0%; Score 201; DB 5; I
 112 CSQNBYFDSLLHACIPCQLRCSSNTPPLTCQRYC 145
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 Disclosure; Page 189-190; 389pp; English.
 (CONF-) CONFORMA THERAPEUTICS CORP.
 AAB60699 standard; protein; 302 AA
 01-MAR-2002; 2002WO-US006518.
 01-MAR-2001; 2001US-0272751P.
 (revised)
(first entry)
 34; Conservative
 Fritz LC, Burrows FJ;
 WPI; 2002-698710/75.
 Local Similarity
 N-PSDB; ABS73235
 Sequence 288 AA;
 WO200269900-A2
 Homo sapiens
 12-SEP-2002
 11-SEP-2003
22-MAY-2001
 AAB60699;
 Query Match
 Matches
 RESULT
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1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34

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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the remained of a variety of immune-related disorders. BAFF-R is a member of the TWE (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. Cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. B-cell lymphoproliferative disorders, hypertension and renal disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R coll growth and maturation it is useful for treating diseases conclused signed and prometrial and maturation in the superful careting diseases conclus systemic lupus erythematosus, autoimmune haemolytic anaemia, cave's disease, multiple myelome, B-cell carcinoman, learned, in man BAFF, hereby inhibiting inflammation. The BAFF-R proteins or BAF
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; becall maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; b-cell carcinoma; lenkaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
 human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents the BAFF-R fusion protein BAFF-R-Fc, comprising a mouse IgG-kappa signal sequence, residues 1-153 of human BAFF-R and a human IgG Fc sequence. (Updated on 11-SEP-2003 to
Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
 Schneider P;
 Browning J, Ambrose C, Tschopp J,
 Example 4; Fig 2; 59pp; English.
 17-AUG-1999; 99US-0149378P.
11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
 16-AUG-2000; 2000WO-US022507
 (BIOJ) BIOGEN INC. (APOT-) APOTECH R & D SA.
 WPI; 2001-202866/20.
 N-PSDB; AAF59999
 WO200112812-A2.
 Homo sapiens
 22-FEB-2001.
 Mackay F, E
Thompson J;
 Mus sp.
Chimeric.
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Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the
 gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLB; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; tumour anapplanteation; HIV; human immunodeficiency virus; TNF; murine; tumour necrosis factor; B cell maturation protein; BCMA; fusion protein; immunoglobulin G; IGG; Fc region.
 Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic;
 23. .302
/Label= Mature_human_BCMA_IgG_Fc_fusion_protein
 /note= "Derived from murine Ig kappa sequence"
 Cachero T, Ambrose C, Rennert P;
 /note= "Derived from human IgG Fc region"
 .75
.e= "Derived from human BCMA protein"
 Human BCMA-Immunoglobulin G Fc region fusion construct.
 24. .302
/label= Cysteine rich domain
/note= "Derived From human BCMA"
CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 64
 l. .22
/label= Signal_peptide
 Location/Qualifiers
 Example 1; Fig 3B; 85pp; English.
 AAE00507 standard; protein; 302
 06-OCT-1999; 99US-0157933P.
11-FEB-2000; 2000US-0181807P.
30-JUN-2000; 2000US-0215688P.
 05-OCT-2000; 2000WO-US027579
 (first entry)
 Schneider P, Thompson J,
 (APOT-) APOTECH R & D SA
 'note=
 (revised)
 WPI; 2001-266242/27.
 BIOJ) BIOGEN INC.
 N-PSDB; AAD03847
 WO200124811-A1.
 Homo sapiens.
 11-SEP-2003
 12-APR-2001
 antagonist
 AAE00507;
 31
 Chimeric
 Protein
 Protein
 gg
 Region
 Domain
 Region
 Mus
 RESULT
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ch 100.0%; Score 201; DB 4; Length 302; Similarity 100.0%; Pred. No. 2.1e-17; 34; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity

Best Loca Matches

Sequence 302 AA;

The invention relates to a novel method for treating a neurodegenerative

Claim 12; Page 70-71; 72pp; English.

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useful for treating undesired cell proliferation such as cancer or carcinoma. e.g. human lung carcinoma, colon carcinoma breast carcinoma, castonema e.g. human lung carcinoma, orlon carcinoma, breast carcinoma, prostate carcinoma, wand other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autoimmune diseases (Grave's clasease, systemic lupus erythematosus-SLB); hypertension, cardiovascular diseases, renal disorders, B-cell lympho-proliferative disorders, cimmunosuppressive diseases, organ transplantation, inflammation and human immune response involving a signalling pathway between APRIL-R and its ligand. APRIL-R DNA is also useful in gene therapy. The present sequence is a fusion construct containing human APRIL-R also referred as BCMA or sequence from murine Ig kappa cDNA. (Updated on 11-SEP-2003 to
 ö
 Treating a neurodegenerative immunological disorder, e.g. demyelination or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
 human; neurodegenerative immunological disorder; demyelination;
Central Nervous System; CNS; inflammation; B-cell maturation antigen;
BCMA; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
 Gaps
 ö
 Length 302;
 Indels
 l. .23
/note= "Murine IgGkappa signal sequence"
 "Human BCMA extracellular domain"
 75. .302
/note= "Human Ig heavy chain Fc region"
 ö
 100.0%; Score 201; DB 4;
100.0%; Pred. No. 2.1e-17;
ive 0; Mismatches 0;
 Human B-cell maturation antigen-Fc SEQ ID NO:3.
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 CSONEYPDSLLHACIPCOLRCSSNTPPLTCQRYC 64
 Location/Qualifiers
 ADG43717 standard; protein; 302 AA.
 21-FEB-2002; 2002US-0358427P.
 21-FEB-2003; 2003WO-US005147
 (first entry)
 34; Conservative
 24. .74
 /note=
 WPI; 2003-721758/68
 gene therapy; mouse
 Kalled SL, Reid H;
 (BIOJ) BIOGEN INC.
 Query Match
Best Local Similarity
 N-PSDB; ADG43718.
 Sequence 302 AA;
 WO2003072713-A2
 Chimeric.
Homo sapiens.
 26-FEB-2004
 04-SEP-2003
 ADG43717;
 Mus sp.
 Region
 Region
 Region
 Matches
 RESULT 27
 Ke.
 ADG4371
 8X9C9C9C9C9C9C5CX8
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immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand (the mammal has or is at risk of developing multiple sclerosis). The method of the invention has neuroprotective, nootropic, and antilnflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence is used in the exemplification of the
 ö
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 immune-related disorder; Becell growth inhibitor; BCMA; B-cell maturation inhibitor; BCMA; B-cell maturation inhibitor; BCMA; B-cell maturation inhibitor; munoglobulin production inhibitor; autoimmune disorder; breal disorder; bypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; plasmid pJST535.
 The invention relates to the use of a BAFF receptor (BAFF-R, also known
 Gaps
 Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 ö
 Length 302;
 Browning J, Ambrose C, Tschopp J, Schneider
 Indels
 100.0%; Score 201; DB 7;
100.0%; Pred. No. 2.1e-17;
ive 0; Mismatches 0;
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
 31 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 64
 AAB60700 standard; protein; 157 AA
 Example 1; Fig 3; 59pp; English.
 17-AUG-1999; 99US-0149378P.
11-FEB-2000; 2000US-0181684P.
18-FEB-2000; 2000US-0183536P.
 16-AUG-2000; 2000WO-US022507
 (first entry)
 Local Similarity 100.0
 (BIOJ) BIOGEN INC.
(APOT-) APOTECH R & D SA.
 WPI; 2001-202866/20.
 N-PSDB; AAF60000
 Sequence 302 AA;
 WO200112812-A2
 Homo sapiens.
 22-MAY-2001
 22-FEB-2001.
 Thompson J;
 nvention.
 Mackay F,
 AAB60700;
 Query Match
 Matches
 RESULT 28
 AAB60700
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Disclosure; Fig 4; 362pp; English.

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treatment of a variety of immuneral protein as an asun to the treatment of a variety of immuneral by the content of a variety of immuneral by the content of an ember of the TMF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases inhibits B-cell growth and maturation it is useful for treating diseases cauch as systemic lupus erythematosus, autoimmune haemolytic anaemia, rapidly human BAFF-B may be allomerulomebhitis, and lymphomas, lenkaemia, rapidly human BAFF-B may be allomerulomebhitis, and lymphomas, lenkaemia, rapidly human BAFF-B may be allomerulomebhitis, and lymphomas, lenkaemia, rapidly human BAFF-B may be allomerulomebhitis, and lymphomas may be encoding
 human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents a human BAFF-R protein sequence as encoded by plasmid PUST535. However, this BAFF-R protein sequence is 27 amino acids
BCMA) protein, or a BAFF-R fusion protein as an agent for the
 shorter than that given in AAB60698
```

Gaps 3; Score 159.5; DB 4; Length 157; Pred. No. 2.1e-12; 0; Mismatches 0; Indels 3; .. 7 QNEYFDSLLHACIPCQLR---NTPPLTCQRYC 35 3 QNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34 79.4%; 29; Conservative Query Match Best Local Similarity Matches 9 ò

Sequence 157 AA;

1;

ADI53060 standard; peptide; 26 AA (first entry) 22-APR-2004 ADI53060; 

protein co-ordinate data, cytostatic; antiallergic; immunosuppressive; antirheumatic; antiarthritic; neuroprotective; antiinflammatory; antiathratic; antiasthmatic; neutrokine-alpha; crystallography; cancer; allergic disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes; systemic lupus erythematosus; asthma; receptor.

Human BCMA receptor binding site.

Homo sapiens

WO2003050134-A2 19-JUN-2003. 07-NOV-2002; 2002WO-US035661.

(HUMA-) HUMAN GENOME SCI INC. 07-NOV-2001; 2001US-0331049P

Volovik Y; Li Y, Oren DE, Arnold E,

WPI; 2003-532895/50.

New crystalline Neutrokine-alpha protein, useful for designing compounds that bind, inhibit or mimic a Neutrokine-alpha protein or enhance the activity of a Neutrokine-alpha protein for treating e.g. cancer or allergic disorders.

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The invention relates to a neutrokine-alpha protein in crystalline form. The crystalline neutrokine-alpha protein is useful for designing molecules that have biological activity or compounds that bind, inhibit or minic a neutrokine-alpha protein and/or enhance the activity of a neutrokine-alpha protein. The three-dimensional structure of a neutrokine-alpha protein in determining the three-dimensional of other neutrokine-alpha proteins and their homologs. The compounds that minic, prevent or inhibit the activity of the protein are useful for treating cancer, allergic disorders, or autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus erythematosus or asthma. This sequence represents the residues in the
 ö
 The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to identify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses a
 BCNA, necrosis factor-kB activator; NP-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
 Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
 Gaps
 ö
 Length 26;
 Indels
 47. .72
/note= "putative transmembrane domain"
 ö
 Score 151; DB 7; I
Pred. No. 4.2e-12;
 Amino acid sequence of murine BCMA polypeptide.
 75.1%; Scot.
100.0%; Pred. No. ...
0; Mismatches
 receptor for binding a cytokine ligand.
 5 EYFDSLLHACIPCQLRCSSNTPPLTC 30
 EYFDSLLHACIPCQLRCSSNTPPLTC 26
 Location/Qualifiers
 AAB08844 standard; peptide; 185 AA.
 Claim 32; Fig 7B; 53pp; English.
 99US-0121485P.
 24-FEB-2000; 2000WO-US004925
 02-JAN-2001 (first entry)
 (GEHO) GEN HOSPITAL CORP.
 26; Conservative
 WPI; 2000-558405/51.
 Query Match
Best Local Similarity
Matches 26; Conserv
 Seed B, Ting A;
 Sequence 26 AA;
 WO200050633-A1
 Mus musculus
 24-FEB-1999;
 31-AUG-2000
 expression.
 Domain
 RESULT 30
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recombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
 The present invention relates to Tumour necrosis factor (TNF) and Apolrelated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for requiating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte
 Muxine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1; Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLB; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; hemeolytic anaemia; Grave's disease; mysathenia gravis; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation; post-streptococcal glomerulonephritis; polyarteritis nodosa.
 Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
 ..
7
 67.7%; Score 136; DB 3; Length 185; 70.6%; Pred. No. 2.5e-09; ive 2; Mismatches 6; Indels
 Murine B cell maturation factor (BCMA) protein.
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
 CEHSEYFDSLLHACKPCHLRCSN--PPATCOPYC 36
 Claim 37; Page 107-108; 112pp; English.
 (NAJE-) NAT JEWISH MEDICAL & RES CENT
 AAY71980 standard; protein; 185
 05-MAY-2000; 2000WO-US012266
 99US-0132892P
 01-MAY-2000; 2000US-0201012P
 (first entry)
 Local Similarity 70.6
 WPI; 2001-016094/02.
 N-PSDB; AAD02130.
 Sequence 185 AA;
 WO200068378-A1
 06-MAY-1999;
 Mus musculus
 28-MAR-2001
 16-NOV-2000.
 designing
 AAY71980;
 Query Match
 Shu HS;
 RESULT 31
AAY11980
1D AAY7
XX AAY7
XX AAY7
XX AAY7
XX AAY7
XX AAY7
XX AMX1
XX MUX
XX MUX
XX HORT
XX AMPI
XX C18
XX
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associated autoimmune disorders like rheumatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding nucleic acid sequence are also useful in diagnostic assays. The present sequence is a murine B cell maturation factor (BCMA). BCMA is
 The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell
 Mouse; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; Pymphoproliferatine disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; coron; a disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis;
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 Gaps
 .
7
 67.7%; Score 136; DB 4; Length 185; 70.6%; Pred. No. 2.5e-09;
 Indels
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
 CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36
 Pred. No. 2.5e
2; Mismatches
 Mouse B cell maturation (BCMA) protein.
 AAE15490 standard; protein; 185 AA
 Disclosure; Fig 11; 94pp; English.
 the receptor for TALL-1 protein
 27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567.
 12-MAY-2000; 2000US-0204039P.
 70.68;
 12-MAR-2002 (first entry)
 24; Conservative
 WPI; 2002-066686/09.
 Best Local Similarity
Matches 24; Conserv
 (AMGE-) AMGEN INC.
 Sequence 185 AA;
 WO200187979-A2.
 22-NOV-2001
 rheill LE,
 AAE15490;
 Query Match
 g
 ligand
 Mus
 AAE15490
 88888888888888
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Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; proteste; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; coron's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HVV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
 Gaps
 7
 Length 185;
 Mouse BCMA-human immunoglobulin Fc region fusion protein.
 Indels
 .,
 67.7%; Score 136; DB 5;
70.6%; Pred. No. 2.5e-09;
iive 2; Mismatches 6.
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
 CFHSEYFDSLLHACKPCHLRCSN--PPATCOPYC 36
 AAE15489 standard; protein; 281 AA
 Disclosure; Fig 10B; 94pp; English.
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567
 (first entry)
 24; Conservative
 is mouse BCMA protein
 (revised)
 WPI; 2002-066686/09.
 Local Similarity
 (AMGE-) AMGEN INC.
 Yu G;
 Sequence 185 AA;
 WO200187979-A2.
 Homo sapiens.
 29-AUG-2003
12-MAR-2002
 22-NOV-2001
 rheill LE,
 AAE15489;
 Chimeric.
 Query Match
 Matches
 RESULT 33
 AAE15489
 8x8888888888x8
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering

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specific binding partner for APRIL (G70, a tumour necrosis factor-TNP family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI (Imphoproliferative disorders, one or more solid tumnours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (crown's disease, clerosis, rheumatoid arthritis, softenderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is mouse BCMA protein-human immunoglobulin Fc region fusion protein.
 ä
 systemic lupus erythematosus; B-cell-mediated cancer; lymphoma; inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis; Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
 glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis; multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
 The invention relates to a novel TALL-1-binding polypeptide comprising defined sequence in the specification. The composition is useful in modulating the activity of TALL-1, and in treating, preventing, ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune
 New TALL-1-binding polypeptide, useful for modulating the activity of TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune diseases, cancers or lymphomas.
 Gaps
 TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
 5
 Length 281;
 Indels
 9
 Score 136; DB 5;
Pred. No. 3.8e-09;
2; Mismatches 6
 CFHSEYFDSLLHACKPCHLRCSN--PPATCOPYC 36
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 TALL-1 related protein SEQ ID No 197.
 Disclosure; Page 26; 236pp; English.
 ABJ38417 standard; protein; 42 AA
 67.7%;
70.6%;
 13-MAY-2002; 2002WO-US015273.
 11-MAY-2001; 2001US-0290196P
 Query Match
Best Local Similarity 70.55
These 24; Conservative
 12-JUN-2003 (first entry)
 WPI; 2003-156719/15.
 (AMGE-) AMGEN INC.
 Sequence 281 AA;
 WO200292620-A2
 Hen H;
 gene therapy.
 Homo sapiens.
 21-NOV-2002
 ABJ38417;
 Min H,
 RESULT 34
 ABJ3841
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disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or lymphoma. The composition may also be used in treating inflammations (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease, asthma, atherosolerosis, cachexia, cirrhosis, diabetes, glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple myeloma, multiple sclerosis, osteoporosis, parkinson's disease, psoriasis and vaculitis. Disorders may be treated with the novel composition using gene therapy. This sequence represents a TALL-1 related protein of the
 Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; coron; a disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; mouse.
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 ๙
 The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/
 Gaps
 Human-murine B cell maturation protein (BCMA) consensus sequence.
 ö
 61.7%; Score 124; DB 6; Length 42; 100.0%; Pred. No. 1.9e-08; ive 0; Mismatches 0; Indels
 AAE15491 standard; protein; 117 AA
 Disclosure; Fig 11; 94pp; English.
 1 CSQNEYFDSLLHACIPCQLRC 21
 CSONEYFDSLLHACIPCOLRC 42
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567.
 (first entry)
 21; Conservative
 (revised)
 WPI; 2002-066686/09.
 Similarity
 (AMGE-) AMGEN INC.
 Yu G;
 Sequence 42 AA;
 WO200187979-A2.
 Homo sapiens
 29-AUG-2003
12-MAR-2002
 22-NOV-2001.
 Theill LE,
 Invention
 AAE15491;
 Chimeric.
 Query Match
 Local
 ligand.
 gg
 Matches
 AAE1549
 888888888888
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BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/Orn BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammatoria, mod immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease, drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human-murine B cell maturation protein (BCMA) consensus sequence. (Updated on 29-NUG-2003 to standardise OS field)
 4.
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 Human; transmembrane activator and intracellular CAML interactor; TACI, cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia, asthma; inflammatory bowel disease; crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 Gaps
 7;
 Length 117;
 Human-murine BCMA consensus sequence cysteine rich region.
 Indels
 46.5%; Score 93.5; DB 5;
69.7%; Pred. No. 0.00042;
iive 1; Mismatches 2;
 2 SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 2 AQCEYPDSLIHAC-PC-LRCS----PPTCQ-YC 27
 rheumatoid arthritis; atherosclerosis; mouse.
 AAE15492 standard; peptide; 24 AA.
 Disclosure, Fig 11; 94pp; English.
 2000US-0204039P.
2000US-0214591P.
2001US-00214591.
 14-MAY-2001; 2001WO-US015567
 Query Match
Best Local Similarity 69...
Best Local Similarity 69...
 (first entry)
 (revised)
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
 Ϋ́α G;
 Sequence 117 AA;
 WO200187979-A2.
 Homo sapiens
 12-MAY-2000;
 27-JUN-2000;
 14-MAY-2001;
 29-AUG-2003
12-MAR-2002
 22-NOV-2001
 rheill LE,
 Chimeric.
 AAE15492;
 ligand
 RESULT 36
 AAE15492
 888888888888888888888888
 8
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consenus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. In memmal which is useful for inhibiting activity of TACI and/or BCMA, in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting including activity of TACI and/or BCMA in a mammal which is useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (athma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human-murine B cell maturation protein (BCMA) consensus sequence cysteine rich region. (Updated on 29-AUG-2003 to standardise OS field)
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45.0%; Query Match Best Local Similarity Sequence 24 AA;

7; Score 90.5; DB 5; Length 24; Pred. No. 0.0002; 0; Mismatches 1; Indels 5 EYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34 22; Conservative Matches 셤 à

4

Gaps

AAY94006 standard; protein; 249 AA AAY94006;

A murine ztnf4, a tumour necrosis factor ligand (first entry)

20-OCT-2000

Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAMI-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autotimune disease; amyloidosis; systemic lupus erythematosus; mysthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; renal neoplasm; multiple myelonephritis; vasculitis; nephritis; renal neoplasm; multiple myelonephritis; vasculitis; nephritis; immune response; immunosuppression; graft rejection; joint pain; immune response; imflammation; swelling; anamia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli. 

Mus musculus.

WO200040716-A2.

13-JUL-2000.

07-JAN-2000; 2000WO-US000396.

07-JAN-1999; 99US-00226533 (ZYMO) ZYMOGENETICS INC

Xu W, Madden K, Gross JA,

DP;

Yee WPI; 2000-452538/39.

N-PSDB; AAA58566

Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases,

The present sequence represents murine ztnf4, a tumour necrosis factor ligand. The extracellular domains of BR43x2 (an isoform of the transmembrane activator and CAML-interactor (TACI) receptor). TACI or transmembrane activated ocutain a cysteine rich domain, and are used for inhibiting ztnf4 activity. They may also be used for inhibiting RR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. Present is associated with asthma, bronchitis, emphysema, end stage renal failure, glomerulonephritis, vasculitis, onephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, amyloidosis, moderating immune response, immunosuppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, inflammation, insulin dependent diabetes mellitus, crohn's disease, point polypeptides, fusions, antibodies, agonists or actousion, and cholesterol renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide. Gaps 1; 35.6%; Score 71.5; DB 3; Length 249; 35.3%; Pred. No. 0.57; Indels 13; 8; Mismatches Disclosure, Page 163; 175pp; English. Local Similarity 35.3 nes 12; Conservative Sequence 249 AA; or renal emboli Query Match Best Loca Matches 

1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34 | :::|:|| : |: | | : | : | : | : | CPKDQYWDSSRKSCVSCALTCSQRS-QRTCTDFC 38 ð

RESULT 38

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ADC71568 standard; protein; 1548 AA

ADC71568;

(first entry) 18-DEC-2003 Mouse subtilisin-like protein convertase 6 (SPC6).

neuroleptic; subtilisin-like protein convertase 6 agonist; subtilisin-like protein convertase 6 antagonist; transgenic; subtilisin-like protein convertase 6; SPC6; schizophrenia.

Mus sp.

US2003093824-A1.

15-MAY-2003

25-JUN-2002; 2002US-00180903.

26-JUN-2001; 2001US-0300978P. 24-SEP-2001; 2001US-0324820P.

(ALLE/) ALLEN K D.

Allen KD;

WPI; 2003-777261/73. N-PSDB; ADC71567.

therapeutic agents for treating a variety of diseases, including schizophrenia, comprises a disruption in a subtilisin-like protein New transgenic mouse useful in methods for identifying potential convertase 6 (SPC6) gene 

expressed in kidney (renal cell adenocarcinoma), head and neck tissue,

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 Subtilase; chromosome 9q21.13; EST; expressed sequence tag; kidney; renal cell; head; neck; heart; multiple sclerosis; lesion; cervix; pooled germ cell; tumour; uterus; adenocarcinoma; retina II; stomach; proprotein convertase subtilisin; furin-like repeat; Alzheimer's disease; Parkinson's disease; pain; colon; pelvic pain; pre-oesophageal dysphagia; gastritis; ulcers; urinary incontinence; lupus nephritis; renal transplant rejection; myocardial infarction; erectile dysfunction; ovary; lung; thyroid; carcinoma; lymphoma; Rapoal's sarcoma; congestive heart failure; ischaemia; hypertensive vascular disease.
 New subtilase-encoding polynucleotide and its encoded protein, useful for identifying modulators of subtilase activity, and in gene therapy for treating e.g. Alzheimer's disease, cancers, congestive heart failure or
 invention describes a transgenic mouse (I) comprising a disruption in
 an subtiliain-like protein convertage (SPC6) gene, where there is no native expression of an endogenous SPC6 gene. The therapeutic agent is administered by inhalation or insufficiation or ral, buccal, parenteral, topical, subcutaneous, intraperitoneal, intravenous, intrapleural, intravenous, intrapleural, intravenous, intrapleural, intravenous, intrapleural, intravenous, intrapleural, sesociated methods are useful for identifying potential therapeutic agents (e.g. SPC6 agonists and antagonists) for treating conditions associated with SPC6. The identified agents are potentially useful for treating diseases such as schizophrenia. The mouse is useful for equence of mouse SPC6. This is the amino acid
 Gaps
 5.
 DB 7; Length 1548;
 Score 67.5; DB 7; Length 1:
Pred. No. 12;
4; Mismatches 14; Indels
 CSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQR 32
 Disclosure; Page 122-26; 135pp; English
 Disclosure; SEQ ID NO 2; 34pp; English.
 ABB80243 standard; protein; 1877 AA.
 15-JAN-2002; 2002US-0347876P.
29-JUL-2002; 2002US-0398734P.
 33.6%;
 14-JAN-2003; 2003WO-EP000253
 Query Match

Query Match

Best Local Similarity 37.00,

Best Local 14; Conservative
 (first entry)
 WPI; 2003-608065/57.
 Sequence 1548 AA;
 Murine subtilase.
 AG
 WO2003060109-A2.
 (FARB) BAYER
 Mus musculus
 04-DEC-2003
 24-JUL-2003.
 Koehler RH;
 ABB80243;
 ischemia
 RESULT 39
 ABB80243
8
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This sequence shows a murine subtilase. The homologous human subtilase coding sequence is located on chromosome 9q21.13. Related EST's are

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chart, multiple sclerosis lesions, cervix, pooled germ cell tumours, chart, multiple sclerosis lesions, cervix, pooled germ cell tumours, uterus tumour, adenocarcinoma, retina II and stomach. The subtilisin protein is a long membrane bound protein which shows 96% identity to human proprotein convertase subtilisin. There are two blocks of 11 furinise repeats in the C-terminal portion. Of the protein. It has one can seminate domain, also in the C-terminal portion. Suggesting that the protein is localised on the outside of the membrane. The subtiliase polynucleotide and polypeptide are useful for identifying test compounds, which may act as agonists or antagonists at the receptor site and which can be regulated to provide therapeutic effects. Vectors comprising the polynucleotide are useful for modulating the activity of subtiliase in a seminar in never a cardiovascular disorder, a gentrointestinal disorder, cancer, a cardiovascular disorder, a gentrointestinal disorder, cancer, a cardiovascular disorder, a gentrointestinal chabetes. In particular, these diseases are Alzheimer's disease, cancer, a cardiovascular disorder, a gentrointestinal cransplant rejection, paln, colon tumour, pre-oesophageal dysphagia, gastritis, ulcers, urinary incontinence, lupus nephritis, renal cransplant rejection, paln, colon tumour, kapenicin, ovary tumour, corribed subsetting or tangettive heart failure, myocardial infarction, ischaemia, hypertensive vascular diseases, etc. These are also useful for preventing or ameliorating the diseases cited above
 ä
 cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; prophoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atheroselerosis.
 Human; transmembrane activator and intracellular CAML interactor; TACI;
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by
 Gарв
 5.
 DB 7; Length 1877;
 Score 67.5; DB 7; Length 1
Pred. No. 14;
4; Mismatches 14; Indels
 1481 CAAVEYWDEGSHRCQPCHKKCSRCSGPSEDQCYTCPR 1517
 1 CSONEYFDSLLHACIPCOLRCSSNTPP----LTCOR 32
 Human TACI cysteine-rich consensus region #1.
 AAE15495 standard; peptide; 33 AA
 2000US-0204039P.
2000US-0214591P.
2001US-00214591.
 33.6%;
 14-MAY-2001; 2001WO-US015567
 12-MAR-2002 (first entry)
 0.0 Query Match
Best Local Similarity 37.8
Matches 14; Conservative
 WPI; 2002-066686/09
 (AMGE-) AMGEN INC.
 Sequence 1877 AA;
 Yu G;
 WO200187979-A2
 Ното варіенв.
 12-MAY-2000;
27-JUN-2000;
 14-MAY-2001;
 22-NOV-2001
 Theill LE,
 AAE15495;
 RESULT 40
 AAE15495
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1;
administering a binding partner for APRIL, a tumor necrosis factor family
 diseases such as diarrhoea, poriasis, allergies, pneumonia, atopic demartitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, collitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protoxoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human TACI cysteine-rich consensus region
 The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering specific binding partner for APRIL (G70, a tymour necrosis factor-TNF)
 post-streptococcal glomerulonephritis; polyarteritis nodosa; TACII; CRD; cysteine rich domain.
 family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or ECMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function
 TALL-1; antagonist; immunosuppressive; antirheumatic; antinflammatory; antiathritic; dermacological; antidabetic; neuroprotective; antithyroid; antipyretic; nephrotropic; vasotropic; vaccine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; Goddpasture's syndrome; pemphigus vulgaris; acute rheumatic fever;
 Gaps
 1;
 cch 33.1%; Score 66.5; DB 5; Length 33; 11 Similarity 32.4%; Pred. No. 0.32; 11; Conservative 8; Mismatches 14; Indels
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 ADA49368 standard; peptide; 33 AA
 Human TACI1 cysteine rich domain.
 Claim 1; Fig 12B; 94pp; English
 Xu L;
 24-OCT-2001; 2001US-0345106P.
14-JMN-2002; 2002US-034896ZP.
07-FEB-2002; 2002US-0354966P.
13-AUG-2002; 2002US-0403334P.
 24-OCT-2002; 2002WO-US034376
 (first entry)
 Liu Y,
 Query Match
Best Local Similarity
 Shu H,
 WO2003035846-A2.
 Sequence 33 AA;
 Homo sapiens
 20-NOV-2003
 01-MAY-2003
 ADA49368;
 Zhang G,
 ligand
 Best Loca
Matches
 RESULT 41
ADA49368
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The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &byr; strands CO and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antirheumatic, neuroprotective, antithyroid, antipyretic, nephrotropic, and vasotropic activity. TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal. TC is useful for inhibiting TALL-1 biological activity in a mammal. TC is useful for inhibiting TALL-1 diseases, rheumatoid arthritis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, mysethaenia gravis, carve's disease, autoimmune hemolytic anaemia, autoimmune companie, purpura, Godpasture's syndrome, pemphigus vulgaris, acute rheumatic fever, post-streptococcal glomerulonephritis and acute trick present sequence represents a cysteine rich
 dermatological; neuroprotective; nootropic; immunomodulator; metabolic; antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; antiparklinsonian; antipsoriatic; vasotropic; antibacterial; asthma; AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor; mesenteric lymph node; AGP-3R; inflammatory disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn's disease; pancreatitis; amtyotrophic lateral solerosis; ALS; Alzhaimer's disease; diabetes; glomerulonephritis; inflammatory bowel disease; ischaemia;
 Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biologiactivity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
 Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 1;
 33.1%; Score 66.5; DB 6; Length 33; ilarity 32.4%; Pred. No. 0.32; Conservative 8; Mismatches 14; Indels
 multiple sclerosis; Parkinson's disease; transgenic animal.
 Human AGP-3 receptor cysteine rich repeat region #1.
 1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
 1 CPEEQYWDPLLGTCMSCKTICNHOS-ORTCAAFC 33
 Disclosure; Page 617; 618pp; English.
 domain (CRD) module of human TACII.
 AAU10951 standard; protein; 37 AA
 12-FEB-2001; 2001WO-US004568
 11-FEB-2000; 2000US-0181800P
 12-MAR-2002 (first entry)
 WPI; 2003-403345/38
 Local Similarity
les 11; Conserv
 (AMGE-) AMGEN INC.
 Sequence 33 AA;
 WO200185782-A2.
 Homo sapiens.
 15-NOV-2001
 antagonist
 AAU10951;
 Boyle WJ,
 Query Match
 Matches
 RESULT 42
 AAU10951
8
 g
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the invention features to a composition (1) compitating Avr-3 receptor (tumour necrosis factor ligand family member) related protein (II) a useful for modulating AGP-3-related activity in mesenteric lymph nodes (MIM) of a mammal. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins contacted to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3R proteins. (II) is also useful for identifying intracellular proteins that interact with the respective cytoplasmic domains by yeast two-hybrid screening process. (II) is also useful conde, spleen, and Peyer's patches. AGP-3R agonists and antagonists involved in B cell growth, survival and activation particularly in lymph node, spleen, and Peyer's patches. AGP-3R agonists and antagonists of dentified using (II) are used for modulating B cell response and are used to treat diseases characterised by inflammatory processes or deregulated immune response such as rheumatoid arthritis, graft-versus-chost disease, Crohn's disease, lupus, etc. (II) is also useful in the production of hybridoma cells with (II). (II) is useful in the treatment of inflammatory conditions of joints, e.g., rheumatoid arthritis, osteoarthritis, etc. (II), its agonists or antagonists are useful for treating acute pancreatitis, amyotrophic lateral sclerosis (ALS), Alzheimer's disease, asthma, atherosclerosis, cachexia/anorexia, ischaemic injury including cerebral ischaemia, multiple myeloma, multiple celebrosis, etc. The nucleic acids are also useful for producing the companient of the study of in vivo biological activity The propressing (II), which are useful for developing treaser and for the study of in vivo biological activity. The
 Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor ligand family member) receptor and encoding nucleic acids.
 The invention relates to a composition (I) comprising AGP-3 receptor (tumour necrosis factor ligand family member) related protein (II)
 present sequence represents the amino acid sequence of human AGP-3 cysteine-rich repeat region #1
 Claim 1; Fig 18; 124pp; English.
```

ï 33.1%; Score 66.5; DB 5; Length 37; 32.4%; Pred. No. 0.36; Live 8; Mismatches 14; Indels Best Local Similarity 32.4 Matches 11; Conservative Sequence 37 AA; Query Match

1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34 | : : | : | : | : | : | : | : | CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAPC 34

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AAE15500 standard; peptide; 59 AA 

AAE15500;

Human TACI cysteine rich extracellular region.

(first entry)

12-MAR-2002

Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis

Homo sapiens

WO200187979-A2.

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (GTO), a tumour necrosis factor-TNF family ligand), having the consenus region of TACI, BCMA, or the TACI EMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointesitnal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human TACI cysteine-rich extracellular region
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 7
 33.1%; Score 66.5; DB 5; Length 59; 32.4%; Pred. No. 0.58;
 Indels
 8; Mismatches
 Disclosure; Fig 13; 94pp; English
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567
 33.14

Query Match
Best Local Similarity 32.4³

Matches 11, Conservative
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
 Sequence 59 AA;
22-NOV-2001
 Theill LE,
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Gaps 34 1 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 33 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC RESULT 44 8

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AAW75785 standard; protein; 166 AAW75785; 

Human lymphocyte surface receptor extracellular domain. PACI; transmembrane activator and CAML-interactor;

(first entry)

18-JAN-1999

calcium signal-modulating cyclophilin ligand; human; lymphocyte, infection; lymphocyte surface receptor; human; B-cell; B lymphocyte; infection; cancer; rheumatoid arthritis; autoimmune disease; glomerulonaphritis; immunosuppressive; graft versus host disease; transplant rejection; therapy; signal transduction.

Homo sapiens

WO9839361-A1.

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (SEMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (GYO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic diseases uch as diarrhoea, psoriasis, allergies, pneumonia, atopic disease, drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, button and intercosis, cancer soling the skin or organs. The present sequence is the state of the skin or organs. The present sequence
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 is human TACI protein extracellular domain
 Claim 1; Fig 12A; 94pp; English.
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567.
 11; Conservative
 WPI; 2002-066686/09.
 Local Similarity
 (AMGE-) AMGEN INC.
 Yu G;
 Sequence 166 AA;
 Theill LE,
 ADN03188;
 Query Match
 ligand.
 Best Loca
Matches
 46
 RESULT
 6
 셤
 This is the amino acid sequence of the N-terminal, i.e. the extracellular, domain of novel human transmembrane activator and CAML-Interactor (TACI) protein (see AAWY5783). TACI is a lymphocyte receptor protein that is involved in the calcium activation pathway. It is normally present in B-lymphocytes, and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. The extracellular domain of TACI functions as a binding site for a ligand that stimulates the activation of the cell by inducing the binding of the C-terminal portion (see AAW75784) of TACI to the N-terminal domain of CAML. A recombinant form of the extracellular portion of TACI acts as a dominant-negative or blocking agent and acts to suppress the immune system. It can be used to treat or prevent autoimmune disease, graft rejection or graft versus host disease. The extracellular region is also used in a claimed method for identifying a ligand for TACI, in which activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription activation of NF-AT dependent transcription
 ä
 New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.
 14; Indels 1; Gaps
 Score 66.5; DB 2; Length 166;
Pred. No. 1.6;
8; Mismatches 14; Indels 1
 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
 (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL
 AAE15494 standard; protein; 166 AA
 Claim 8; Page 73; 89pp; English.
 Human TACI extracellular domain.
 98WO-US004270.
 33.1%;
32.4%;
 97US-00810572
 12-MAR-2002 (first entry)
 11; Conservative
 Von Bulow G;
 WPI; 1998-506346/43.
 Query Match
Best Local Similarity
 N-PSDB; AAV57330
 Sequence 166 AA;
 03-MAR-1998;
 03-MAR-1997;
11-SEP-1998.
 Bram RJ,
 AAE15494;
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transmembrane activator and CAML interactor; TACI; extracellular domain; trimerising polypeptide; homotrimeric protein complex; antiinflammatory; antiarthritic; antiinflammatory immunosuppressive; antiarteriosclerotic; cytostatic; gene therapy; inflammatory disease; rheumatoid arthritis; inflammatory bowel disease; autoimmune disease; atherosclerosis; osteoporosis; allograft rejection; cancer; human; heat shock binding protein; HSBP; fusion protein.
CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
 Human TACI-HSBP fragment SEQ ID NO:18.
 ADN03188 standard; protein; 171 AA
 15-JUL-2004 (first entry)
 WO2004033486-A2.
 sapiens.
 Synthetic
```

Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; cronh's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis:

WO200187979-A2

22-NOV-2001.

Homo sapiens

1; Gaps

33.1%; Score 66.5; DB 5; Length 166; 32.4%; Pred. No. 1.6; Live 8; Mismatches 14; Indels

Matches

RESULT 45 AAE15494 ID AAE1

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Pitti RM;

Marsters SA,

Kim KJ,

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activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple solerosis, psoriasis and lupus erythematosus. The present sequence is human TACI splice variant protein
 The invention relates to methods of using one or more agonists or antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g. TAC1 or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or
 Human, TACI, BR3, receptor; tumour necrosis factor ligand, TNF ligand,
TALL-1; April; systemic lupus erythematosus.
 Amino acid sequence of an alternatively spliced human TACI receptor.
 Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
 | : : | | | : | : | : | : | CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
 8; Mismatches
 33.1%; Score 66.5; 32.4%; Pred. No. 2.6
 Yan M;
 Grewal I,
 ABP97723 standard; protein; 266 AA
 Example 1; Fig 6; 160pp; English
 Grewal I; Ridgway J,
 16-FEB-2000; 2000US-0182938P.
22-AUG-2000; 2000US-0226986P.
 24-JUL-2002; 2002WO-US023487.
 03-AUG-2001; 2001US-0310114P.
 28-MAY-2003 (first entry)
 Local Similarity 32.4
108 11; Conservative
 Dodge KH,
 (GETH) GENENTECH INC
 (GETH) GENENTECH INC
 WPI; 2001-541628/60.
 WPI; 2003-256560/25
 Sequence 265 AA;
 WO2003014294-A2
 Ashkenazi AJ,
 Homo sapiens
 antagonists.
 20-FEB-2003,
 ABP97723;
 Dixit V,
 Query Match
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Matches
 ían M;
 ABP97723
 RESULT
%X&X&BXBXBXBXBXBXBXBXBXBX
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 comprising the polypeptide; (2) an expension vector comprising the polypeptide; (2) an expension vector comprising the following operably linked elements, a transcription promoter, the nucleic acid sequence encoding the polypeptide, and a transcription terminator; (3) a cultured cell into which has been introduced the expression vector, where the cell expresses the polypeptide; (4) producing a homotrimeric protein complex by culturing the cell, and recovering the homotrimeric protein complex by culturing the Sells to the homotrimeric protein complex. The polypeptide has antiinflammatory, antiarthritic, antiinformatic, immunosuppressive, antiarterisoclerotic and cyrostatic activities, and can be used in gene therapy. The polypeptides are useful for treating and controlling inflammatory diseases, e.g. rheumatoid arthrities or inflammatory bowel disease, autoimmune disease.

Contributed to set opporosis, allograft rejection and cancer. The present sequence represents a human TACI and heat shock binding protein the properties of the present sequence represents a human TACI and heat shock binding protein the properties are the protein present which is used in the exemplification of
 ij
 The present invention describes an isolated polypeptide comprising an extracellular domain of the transmembrane activator and calcium-signal modulating cyclophilin ligand (CAML) interactor (TACI), and a trimerising polypeptide. Also described: (1) a homotrimeric protein complex
 Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.
 New polypeptide comprising an extracellular domain of the transmembrane activator and calcium-signal modulating cyclophilin ligand (CAML) interactor (TACI), and a trimerizing polypeptide, useful for treating
 Gaps
 1,
 Length 171;
 Indels
 14;
 Score 66.5; DB 8;
Pred. No. 1.7;
8; Mismatches 14;
 | : : | | | | : | : | : | : | : | : | CPEEQYWDPLLGICMSCKTICNHQS-QRTCAAFC 38
 1 CSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 Example 4; SEQ ID NO 18; 36pp; English.
 AAE09244 standard; protein; 265 AA
 Human TACI splice variant protein.
 Jaspers SR
 10-OCT-2003; 2003WO-US032878.
 11-OCT-2002; 2002US-0417801P.
 33.1%;
 32.4%;
 (first entry)
 (ZYMO) ZYMOGENETICS INC
 11; Conservative
 inflammatory diseases
 the present invention
 West JW, Brandt CS,
 WPI; 2004-364855/34.
N-PSDB; ADN03187.
 Best Local Similarity
 Sequence 171 AA;
 WO200160397-A1
 19-NOV-2001
 Ното варіепв
 22-APR-2004.
 23-AUG-2001
 AAE09244;
 Query Match
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Matches

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AAAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-AAE0924-

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Gaps

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Indels

14; 34

DB 4; Length 265;

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The present sequence represents an alternatively spliced human TACI polypeptide. The specification also describes BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April bind to the TACI receptor, while TNF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for preparing a composition for treating systemic lupus erythematosus
 The invention relates to a composition (I) comprising AGP-3 receptor (tumour necrosis factor ligand family member) related protein (II) attached to a vehicle protein. (I) is useful for modulating AGP-3-related activity in mesenteric lymph nodes (MLN) of a mammal. (II) is useful in assays to identify cells and tissues that express AGP-3R or proteins related to AGP-3R-related protein and for identifying compounds (agonists or antagonists) that interact with AGP-3R proteins. (II) is also useful
 dermatological; neuroprotective; noctropic; immunomodulator; metabolic; antidiabetic; analgesic; nephrotropic; osteopathic; cytostatic; fever; antidiaterial; antipsortatic; vasotropic; antibacterial; asthma; AGP-3 receptor; tumour necrosis factor ligand family; AGP-3 receptor; rheumatoid arthritis; graft-versus-host disease; immune disorder; rheumatoid arthritis; graft-versus-host disease; Crohn's disease; pancereatitis; amyotrophic lateral sclerosis; ALS; Alzheimer's disease; disbetes; glomerulonephritis; inflammatory bowel disease; ischaemia; multiple sclerosis; Parkinson's disease; transgenic animal.
 Composition, useful for identifying modulator of receptor for treating asthma and glomerulonephritis, comprises AGP-3 (tumor necrosis factor ligand family member) receptor and encoding nucleic acids.
 Gaps
New nucleic acid encoding a TACIs or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus.
 Human; AGP-3; antiinflammatory; antiarthritic; immunosuppressive;
 ij
 33.1%; Score 66.5; DB 6; Length 266; 32.4%; Pred. No. 2.7;
 14; Indels
 1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
 8; Mismatches
 Human AGP-3 receptor extracellular domain.
 AAU10949 standard; protein; 291 AA
 Disclosure; Fig 8; 153pp; English.
 Claim 1; Fig 18; 124pp; English.
 12-FEB-2001; 2001WO-US004568.
 11-FEB-2000; 2000US-0181800P.
 (first entry)
 11; Conservative
 WPI; 2002-049441/06.
 Best Local Similarity
Matches 11; Conserv
 (AMGE-) AMGEN INC
 Boyle WJ, Hsu H;
 Sequence 266 AA;
 WO200185782-A2.
 Homo sapiens
 12-MAR-2002
 15-NOV-2001.
 AAU10949;
 Query Match
 AAU10949
FFXXXXCCCCCXX
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CC for identifying intracellular proteins that interact with the respective cytoplasmic domains by yeast two-hybrid screening process. (II) is choose, spleen, and Peyer's patches. AGP-3R agonists and antagonists and antagonist antago
 TACI; transmembrane activator and CAML-interactor; calcium signal-modulating cyclophilin ligand; human; lymphocyte surface receptor; human; B.cell; B lymphocyte; infection; cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis; immunosuppressive; graft versus host disease; transplant rejection;
 Gaps
 ;
 33.1%; Score 66.5; DB 5; Length 291; 32.4%; Pred. No. 2.9; ive 8; Mismatches 14; Indels 1
 | : : | : | | | | : | : | : | : | CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
 . .166
|abel= Extracellular_domain
 /label= Transmembrane_domain
 187. .294
/label= Cytoplasmic_domain
/note= "Claim 6"
 "TNFR_NGFR motif"
 Human lymphocyte surface receptor TACI.
 Location/Qualifiers
 AAW75783 standard; protein; 293 AA
 "Claim 8"
 97US-00810572
 98WO-US004270
 18-JAN-1999 (first entry)
 .186
 Conservative
 34. .71
 /note=
 /note=
 extracellular domain
 Query Match
Best Local Similarity
Matches 11; Conserv
 Sequence 291 AA;
 Homo sapiens.
 WO9839361-A1.
 03-MAR-1998;
 03-MAR-1997;
 11-SEP-1998
 AAW75783;
 therapy.
 Peptide
 Domain
 Domain
 Domain
 Key
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BY (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX
Bram RJ, Von Bulow G;
XX
WP1; 1998-506346/43.

RP5DB; AAV57328.

XX
New isolated transmembrane activator protein - used to develop products for treating e.g. infections, cancers, autoimmune and inflammatory conditions, transplant rejection or graft-versus-host disease.

XX
This is the amino acid sequence of novel human transmembrane activator cc and CAML-interactor (TAGI) protein, a lymphocyte protein that is involved in the calcium activation pathway. TAGI is normally present in B conditions, transplant respected to specifically regulate B cell responses involved in the calcium activation pathway. TAGI is normally present in B conditions and to a much lesser extent in immature T-lymphocytes, and can therefore be targetted to specifically regulate B cell responses without affecting T cell activity. TAGI cDNA (seeV7328) was isolated condition are all activity. TAGI cDNA (seeV7328) was isolated conditions of TAGI recombinant DNA constructs, unicellular hosts, and contabled to TAGI protein. Methods are claimed for identifying nimunosuppressive drugs that selectively conditions or cancers. It can be blocked to provide contabled to increase immune system activity, e.g. for treating infections or cancers. It can be blocked to provide conditions such as immune complex-induced vascultis, glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II collised are claimed are the ceptor or graft versus host disease trensplant rejection, rheumatoria darbinicial systemic lupus crythematosus, transplant rejection, rheumatoria gravis induced vasculties.
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Gaps

Search completed: January 28, 2005, 19:52:44 Job time : 39.3395 secs This Page Blank (uspto)

Mouse 1gG
Human BCM
Human BCM
Human BCM
Human BCC
Human BCM
Mouse ECM
TALL-1 re
Human BCM
Murine BA
Mouse Ztn
Amino aci
Human BAF
Human STN
Human BAF
Human STN

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Aab60699
Aae15486
Aae15486
Aae15486
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Aae15486
Aae15489
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Abb3184149
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Adb006890
Adv18790
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Abb004897
Abb004897
Aae29224
AAB60699
AAE00507
AAE00507
AAE15485
AAE15486
AAE15489
AAE15489
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AB173206
AB173224
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AAE22266
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AAE22266
AAE22270
AAE32270
 ABR61767
ADK00764
AAE22243
ABR82287
AAO29657
ADB90668
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AAE09240
AAY71914
 AAE15492
ADB90667
AAE35223
ADG42639
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AAE35225
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AAB36312
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1009
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186
576
 286.5
286.5
286.5
286.5
284
201
201
118.1
118.5
116.5
116.5
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Aae09241 Human BCM
Aay1979 Human BCM
Abb60698 Human Bc
Abb61487 Human Bc
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Aae28961 Human Bc
Aae35216 Human Bc
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Add67527 Human Ly1
Add43715 Human Bc
Abcoose Human Gen
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Aab60706 Human Bc
Aab60706 Human Bac
Aab60706 Human Bac
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 Amino aci
Murine B
 ; Search time 196.661 Seconds (without alignments) 335.635 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 MLQMAGQCSQNEYFDSLLHA......CKSLPAALSATEIEKSISAR 184
 Aay71980 |
Aae15490 |
Aae15501 |
Aae15491 |
 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
 Total number of hits satisfying chosen parameters:
 2002273 seqs, 358729299 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
 protein search, using sw model
 2005, 19:37:53
 AAX94001
AAE09241
AAE05241
AAB60698
AAB60698
AAB60696
AAB61694
AAE28961
AAE28961
AAE28961
AAE3696055
ABP60552
ABP60552
ABP60552
ABP60566060
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AAE15501
AAE15491
 AAB08843
 BLOSUM62
Gapop 10.0 , Gapext 0.5
 Geneseq_23Sep04;*

geneseqp1980s;*

geneseqp2000s;*

geneseqp2001s;*

geneseqp2001s;*

geneseqp2003s;*

geneseqp2003s;*

geneseqp2003bs;*
 seq length: 0
seq length: 200000000
 US-10-077-137-1
964
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 Length
 Copyright
 January 28,
 Query
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Murine pr Mouse pro TALL-1R p Amino aci DHBV Pres Human kin Human KPP Probin ty

Human exp Human exp Human exp Human exp

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Human Human

1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

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The present sequence represents a BCMA (not defined) polypeptide. BCMA is a necrosis factor (NF)-kB activator. The method of the invention is used to indentify compounds which modulate BCMA activity (and thus NF-kB activity). The specification describes a method of identifying a learning a library of with a cell which expresses a recombinant anti-cell death gene expression from a promoter. The method the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug
 tra
 BCMA, necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock.
 Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell death gene and reporter gene, and determining alteration in reporter gene
Aao14130 Human
Abb81488 Human
 9 (4) (5) (5)
 77. .77
note= "putative transmembrane domain"
 ALIGNMENTS
 AA014130
 ABB81488
 Location/Qualifiers
 AAB08843 standard; peptide; 184 AA
 Claim 32; Fig 7A; 53pp; English
 Amino acid sequence of human.
 20,00WO-US004925
 99US-0121485P
 വവ
 (first entry)
 (GEHO) GEN HOSPITAL CORP.
 293
293
 WPI; 2000-558405/51.
 1.8
 Seed B, Ting A;
 Sequence 184 AA;
 WO200050633-A1
 24-FEB-1999 N
 24-FEB-2000;
 02-JAN-2001
 Homo sapiens
 31-AUG-2000
 expression.
78.5
 designing
 AAB08843;
 Domain
 AAB08843
ID AAB(
 RESULT 1
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Human; BR43x2; TACI receptor; extracellular domain; BCWA; B cell protein; transmembrane activator and CAMI-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; reand neoplasm; multiple mylomophritis; vasculitis; nephritis; renal neoplasm; multiple myloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.
 The present sequence represents a human BCMA protein, a B cell protein related to transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TMR) receptor. The extracellular domains of BASA22 (an isoform of TACI) TACI or BCMA (a related B cell protein) receptor contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TMF ligand. They may also be used for inhibiting BR43x2, TACI or BCMA receptor-ligand engagement associated with activated or resting B lymphocytes, effector T-cells, or with antibody production. The antibody production is associated with an autoimmune disease selected from systemic lupus erythemacrosus, myasthenia gravis, multiple sclerosis and rheumatoid arthritis. The ztnf4 activity and BR43x2, TACI or BCMA receptor-ligand engagement is associated with asthma, bronchitis, emphysema, end stage renal failure,
 120
 180
 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATBIEKS 180
GESLIISLÄVFVLMFLIRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.
 A human BCMA protein, a B cell protein related to TACI.
 Disclosure; Page 152; 175pp; English.
 Yee DP;
 AAY94001 standard; protein; 184 AA.
 07-JAN-2000; 2000WO-US000396.
 99US-00226533.
 Gross JA, Xu W, Madden K,
 20-OCT-2000 (first entry)
 (ZYMO) ZYMOGENETICS INC
 WPI; 2000-452538/39.
N-PSDB; AAA58559.
 ISAR 184
 WO200040716-A2
 07-JAN-1999;
 Homo sapiens
 13-JUL-2000
 AAY94001;
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Matches 184; Conservative

Similarity

Query Match Best Local S 1 MLQMAGQCSQNBYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

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Gaps

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100.0%; Score 964; DB 3; Length 184; 100.0%; Pred. No. 9.7e-95; ive 0; Mismatches 0; Indels (

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(NAJE-) NAT JEWISH MEDICAL & RES CENT.
 Location/Qualifiers
 AAY71979 standard; protein; 184 AA.
 06-MAY-1999; 99US-0132892P
01-MAY-2000; 2000US-0201012P
 05-MAY-2000; 2000WO-US012266
 (first entry)
 Matches 184; Conservative
 WPI; 2001-016094/02
 Local Similarity
 ISAR 184
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 Sequence 184 AA;
 WO200068378-A1
 Homo sapiens
 28-MAR-2001
 16-NOV-2000
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 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLPRGLE 120
 GLSLIISLAVFVLMFLLERKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 1 MLÓMAGOCSÓNEYFDSLLHACIPCÓLRCSSNTPPPLTCORYCNASVTNSVKGTNAILWTCL 60
glomerulonephritis, vasculitis, nephritis, pyelonephritis, renal neoplasms, multiple myelonas, lymphomas, light chain neuropathy, amyloidosis, muderating immune response, immunosuppression, graft rejection, graft versus host disease, inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA polypeptides, fusions, antibodies, agonists or antagonists can be used to treat hypertension, renal artery stenosis, or occlusion, and cholesterol or renal emboli
 TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma; autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis
 Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
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 Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological activity, for treating autoimmune disorders and cancer, comprises exposing the cells to TALL-1 or APRIL polypeptide agonists or
 The invention relates to methods of using one or more agonists or
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 Length 184;
 Marsters SA,
 Indels
 Score 964; DB 3; I
Pred. No. 9.7e-95;
Mismatches 0;
 Kim KJ,
 Grewal I,
 AAE09241 standard; protein; 184 AA
 Example 2; Fig 2; 160pp; English
 .
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 100.0%;
100.0%;
 16-FEB-2000; 2000US-0182938P.
22-AUG-2000; 2000US-0226986P.
 28-NOV-2000; 2000WO-US032378
 (first entry)
 Query Match
Best Local Similarity 100.
Marches 184; Conservative
 Dodge KH,
 (GETH) GENENTECH INC.
 WPI; 2001-541628/60.
N-PSDB; AAD15902.
 Human BCMA protein,
 ISAR 184
 ISAR 184
 Sequence 184 AA;
 WO200160397-A1
 Ashkenazi AJ,
 Homo sapiens
 19-NOV-2001
 23-AUG-2001:
 TACI; BCMA;
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 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 180
 Tumour necrosis factor and ApoL-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SLB; insulin dependent diabetes mallitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; chromosome 16; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
 activity. TALL-1 and APRIL antagonists are used to block the interaction between APRIL and APRIL attaconists are used to block the interaction between APRIL and TALL-1 with TACI or BCMA. They are useful for treating a mammal suffering from cancer such as leukaemia, lymphoma, myeloma, cancers of lung and colon and autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis, psoriaais and lupus erythematosus. The present sequence is human BCMA protein
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antagonists to modulate the activity of the members of TNF (tumour necrosis factor) especially TALL-1, ARRIL and TNF receptor (FNFR) e.g. TACI or BCMA. The method is useful for treating pathological conditions or diseases associated with increased TALL-1 and APRIL expression or
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 121 YTVEECTCEDCIKSKPKVDSDHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 1 MIQMAGQCSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 Gaps
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 Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
 Length 184;
 0; Indels
 100.0%; Score 964; DB 4; 100.0%; Pred. No. 9.7e-95;
 Human B cell maturation factor (BCMA) protein.

 .62
 label= Extracellular domain

 0; Mismatches
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17-AUG-1999; 99US-0149378P. 11-FEB-2000; 2000US-0181684P. 18-FEB-2000; 2000US-0183536P.

16-AUG-2000; 2000WO-US022507.

WO200112812-A2 Homo sapiens.

22-FEB-2001

```
The present invention relates to Tumour necrosis factor (TNF) and Apol-
related Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules,
proteins (including homologues), and their antibodies. The invention in
particular relates to methods for regulating the interaction between TALL
and TALL-1 receptors (BCMA referred as B cell maturation factor) to
regulate monocyte, macrophage and B lymphocyte mediated immune responses.
TALL-1 protein is useful for identifying compounds that regulate B
lymphocyte proliferation. It is also useful for treating B lymphocyte
associated autoimmune disorders like rheumatoid arthritis, systemic lupus
crythematosus (SLB), insulin dependent diabetes mellitus, multiple
selerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
anaemia, autoimmune thrombocyte/copenia purpura, Goodpasture's syndrome,
pemphigus vulgaris, acute rheumatic fever, post-streptococcal
corresponding nucleic acid sequence are also useful in diagnostic assays.
The present sequence is a human B cell maturation factor (BCMA) protein.
It is the receptor for TALL-1 protein. BCMA gene is located on chromosome
consented the service of the synchroses of the prain, muscle, heart, lung, kidney, pancreas, testis and placenta.
BCMA mRNA is absent in the pro-B lymphocyte stage but its expression
increases with B lymphocyte maturation
 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 9
 1 MLQWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60
 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor; BCMA; b-cell maturation inhibitor; immunoglobulin production inhibitor; autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour.
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 Gaps
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 Isolated TALL-1 protein is used to identify compounds that reguive proliferation, used to treat B lymphocyte associated autoimmune disorders.
 .
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 100.0%; Score 964; DB 4; Length 184; 100.0%; Pred. No. 9.7e-95; ive 0; Mismatches 0; Indels (
 Claim 37; Page 104-105; 112pp; English
 AAB60698 standard; protein; 184 AA
 Human BAFF receptor (BAFF-R).
 (first entry)
 184; Conservative
 Similarity
 ISAR 184
 ISAR 184
N-PSDB; AAD02125.
 Sequence 184 AA;
 22-MAY-2001
 121
 AAB60698;
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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. specific antibodies can be used for inhibiting B-cell growth, dendritic, cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoimmune disorders. B-cell lymphoproliferative disorders, hypertension and renal disorders. B-cell lymphoproliferative coll spreament of autoimmune disorders. B-cell lymphoproliferative disorders in the treatment of immunosuppressive disorders and HIV collection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R collipsions or altering an immune response involving a signalling pathway between BAFF-R and BAFF, thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythematosus, autoimmune haemolytic anaemia, grave's disease, multiple myseloma, B-cell cacids encoding there are specific and lymphomas. Invision of acids encoding there are proper and an analyzing and lymphomas. Invision of the contraction 180
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 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
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 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 1 MIQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVINSVKGTNAILWTCL
 human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The present sequence represents human BAFF-R
 Gaps
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0
 100.0%; Score 964; DB 4; Length 184; 100.0%; Pred. No. 9.7e-95; ive 0; Mismatches 0; Indels C
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 Schneider
 Tschopp J,
 Browning J, Ambrose C,
 Claim 20; Fig 1; 59pp; English.
 Query Match
Best Local Similarity 100.
Matches 184; Conservative
 (APOT-) APOTECH R & D SA.
 WPI; 2001-202866/20.
 (BIOJ) BIOGEN INC.
 ISAR 184
 ISAR 184
 N-PSDB; AAF59998.
 Sequence 184 AA;
 Thompson J;
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GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

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The invention relates to a method of treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma. The method involves administering a composition comprising A proliferation inducing Ligana Receptor (APRIL-R) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(9). This method is useful for treating undesired cell proliferation such as cancer or carcinoma e.g. human lung carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, breast carcinoma, breast carcinoma, prostate carcinoma, breast carcinoma, by APRIL. It is also useful for treating autoimmune diseases (Grave's disease, systemic lupus erythematosus-SIB); hypertension, cardiovascular diseases, ernal disorders, B-cell lympho-proliferation, inflammation and human immunodeficiency virus (HIV), and for treating, suppressing or altering immunodeficiency virus (HIV), and for treating, suppressing or altering con immune response involving a signalling pathway between APRIL-R and its also useful in gene therapy. The present sequence is human APRIL-R also referred as BCMA or BCM protein
 Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R) antagonist.
 Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertenation; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease; B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; tumour necrosis factor; BCMA; B cell maturation protein.
 Length 184;
 Cachero T, Ambrose C, Rennert
 100.0%; Score 964; DB 4;
100.0%; Pred. No. 9.7e-95;
 Human B cell maturation protein (BCMA).
 AAE00506 standard, protein, 184 AA.
 Claim 3; Fig 3A; 85pp; English
 11-FEB-2000; 2000US-0181807P.
 05-OCT-2000; 2000WO-US027579
 Schneider P, Thompson J,
 (first entry)
 (APOT-) APOTECH R & D SA.
 2001-266242/27.
 (BIOJ) BIOGEN INC
 N-PSDB; AAD03844.
 Sequence 184 AA;
 WO200124811-A1.
 Homo sapiens.
 06-0CT-1999;
 31-JUL-2001
 12-APR-2001.
 Query Match
Best Local S:
 AAE00506;
AAE00506
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The present invention describes a human tumour necrosis factor receptor designated Ztnfr12 (I). (I) has cytostatic, immunosuppressive, dematological, antiinflammatory, neuroprotective, antidiabetic, antiinflammatory, neuroprotective, antidiabetic, antiinteumatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimmune disorders such as systemic lupus erychematosus, mysatehenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid
GISLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLICGMANIDLEKSRTGDEIILPRGLE 120
 180
 Novel isolated human tumor necrosis factor receptor polypeptide, termed Zrnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
 neuroprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; unyasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; aethma; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft rejection; Crohn's disease.
 YTVEBCTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 immunosuppressive; dermatological; antiinflammatory; antidiabetic;
 Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
 Human BCMA receptor related protein SEQ ID NO:7.
 Disclosure; Page 135-136; 154pp; English.
 Grant FJ;
 ABB81487 standard; protein; 184 AA.
 2000US-0246449P.
2000US-0257131P.
2001US-0301715P.
 05-NOV-2001; 2001WO-US047018
 29-AUG-2001; 2001US-0315565P
 Gross JA, Xu W, Henne RM,
 02-SEP-2002 (first entry)
 (ZYMO) ZYMOGENETICS INC
 WPI; 2002-508212/54.
 ISAR 184
 ISAR 184
 WO200238766-A2.
 07-NOV-2000;
20-DEC-2000;
 Homo sapiens
 28-JUN-2001;
 16-MAY-2002.
 ABB81487;
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 RESULT 7
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Mismatches

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Similarity

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1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL

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 New genes that are up- or down-regulated in colorectal cancer, useful for diagnosting colorectal cancer in a subject, or for identifying modulators of colorectal cancer-associated proteins and genes for treating colorectal cancer.
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKVTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 GLSLISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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 neoplasms, multiple myelomes, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel diseases, graft-versus host disease, graft rejection and Crohn's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents a protein which is given in the exemplification of the present invention
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 MIQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 Gaps
 metastasis; differential expression; cytostatic;
 .
0
 Length 184;
 Indels
 Metastatic colorectal cancer-associated polypeptide
 100.0%; Score 964; DB 5;
100.0%; Pred. No. 9.7e-95;
ive 0; Mismatches 0;
 ABP54694 standard; protein; 184 AA.
 INC.
RESERVE.
 Claim 8; Page 255; 260pp; English
 diagnosis; gene therapy; vaccine.
 27-FEB-2001; 2001US-0272206P.
02-APR-2001; 2001US-0281149P.
17-APR-2001; 2001US-028455FP.
 27-FEB-2002; 2002WO-US006001
 (first entry)
 EOS BIOTECHNOLOGY
UNIV CASE WESTERN
 Local Similarity 100.
ses 184; Conservative
 Mack DH, Markowitz SD;
 WPI; 2002-698677/75.
 Colorectal cancer;
 ISAR 184
 ISAR 184
 N-PSDB; ABQ81560
 Sequence 184 AA;
 WO200268677-A2
 Homo sapiens.
 30-DEC-2002
 06-SEP-2002
 Query Match
 61
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 (EOSB-) 1
(UYCA-) 1
 Matches
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The present sequence is the protein sequence of a human polypeptide encoded by a gene that exhibits decreased expression in colon cancerderived metastases compared to normal colon tissue. It is an example of claimed polypeptides that are encoded by genes which are differentially expressed in metastatic colorectal cancer cells. Such polypeptides are useful in diagnostic and prognostic assays, for raising antibodies are e.g. in immunotherapy, and in screening for modulator compounds of
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 120
 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 9
 9
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVINSVKGTNAILMTCL
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLPRGLE
 1 MIQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 Human; tumour; B-cell maturation antigen; transmembrane activator; calcium-modulator; cyclophilin ligand-interactor; TACI; gene therapy; neoplasm; chronic lymphocytic leukaemia; lymphopycliferative diaease; non-Hodgkin's lymphoma; light chain gammopathy; inflammation; asthma;
 Gaps
 ;
0
 Length 184;
 Indels
 Score 964; DB 5;
Pred. No. 9.7e-95;
 1. .48
/note= "Extracellular domain"

 .41
 /note= "Cysteine rich region"

 0; Mismatches
 "Antigenic epitope"
 Human B-cell maturation antigen (BCMA).
 Location/Qualifiers
 AAE28961 standard; protein; 184 AA.
 100.0%;
100.0%;
 20-FEB-2001; 2001US-0270274P.
 06-FEB-2002; 2002WO-US003500
 Matches 184; Conservative
 (ZYMO) ZYMOGENETICS INC
 1. .54
/note=
 BCMA; multiple myeloma
 WPI; 2002-723183/78.
N-PSDB; AAD46410.
 Similarity
 therapeutic value
 ISAR 184
 184
 Sequence 184 AA;
 WO200266516-A2
 ISAR
 Kindsvogel W;
 sapiens
 27-JAN-2003
 29-AUG-2002
 AAE28961;
 61
 181
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 Query Match
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 The invention relates to the manufacture of a composition for inhibiting the proliferation of tumour cells. The method involves using an antibody component that binds both the B-cell maturation antigen (BCMA) and the transmembrane activator and calcium-modulator and cyclophilin ligandinteractor (TACI). BCMA and TACI binding antibody compositions are useful for inhibiting proliferation of tumour cells, particularly inhibiting ZTNF4 activity in a mammal associated with increased endogenous antibody
 production or a disorder consisting of neoplasm, chronic lymphocytic leukaemia, multiple myeloma, non-Hodgkin's lymphoma, post-transplantation lymphoproliferative disease or light chain gammopathy or inflammation e.g. asthma. The invention is also useful in gene therapy. The present is
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 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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 Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human;
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 autoimmune disease; systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation; B-cell maturation receptor; BCMA; receptor.
 Gaps
 calcium
 B-cell maturation antigen and transmembrane activator and calciur modulator and cyclophilin ligand-interactor, useful for treating disorders e.g. inflammation or lymphoma.
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 Length 184;
 Indels
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 100.0%; Score 964; DB 5;
100.0%; Pred..No. 9.7e-95;
ive 0; Mismatches 0;
 B-cell maturation receptor (BCMA) protein.
 Disclosure; Page 63; 67pp; English
 AAE35216 standard; protein; 184 AA
 20-MAY-2002; 2002WO-US015910
 24-MAY-2001; 2001US-0293343P
 (first entry)
 Matches 184; Conservative
 (ZYMO) ZYMOGENETICS INC.
 Query Match
Best Local Similarity
 human BCMA protein
 181 ISAR 184
 ISAR 184
 Sequence 184 AA;
 WO200294852-A2
 28-MAY-2003
 Homo sapiens
 AAE35216;
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 The invention relates to fusion proteins comprising transmembrane activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumnour necrosis factor-like protein (ZTNF)2 or ZTNF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammation, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is human B-cell maturation receptor (BCMA) protein used in the invention
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 interactor (TACI)-immunoglobulin fusion protein, for treating cancer o diabetes, comprises a TACI receptor group and an immunoglobulin group.
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 GISLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 Transmembrane activator and calcium modulator and cyclophilin ligand-
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 Gaps
 human; TALL-1; antagonist; immunosuppressive; antirheumatic; antinflammatory; antiarthritic; dermatological; antidiabetic; neuroprotective; antithyroid; antipyretic; nephrotropic; vasotine; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple solerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; goodpasture s syndrome; pemphigus vulgaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCWA.
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 100.0%; Score 964; DB 6; Length 184; 100.0%; Pred. No. 9.7e-95;
 Indels
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 0; Mismatches
 English.
 ADA49361 standard; protein; 184 AA.
 100.08;
 Disclosure; Col 100; 71pp;
 20-NOV-2003 (first entry)
 Best Local Similarity 100.
Matches 184; Conservative
 Gross JA;
 WPI; 2003-148455/14.
 Human BCMA protein.
 181 ISAR 184
 N-PSDB; AADS3754
 Sequence 184 AA;
 WO2003035846-A2
 Homo sapiens
 Rixon MW,
 ADA49361;
 181
 Query Match
 RESULT 11
 ADA49361

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The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &bgr; strands NO:2, by at least one modification in the region connecting &bgr; strands D and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antirheumatic, antiinflammatcry, antiathritic, neptrobic; and vasotropic activity. A TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 conformation a vaccine. A protein of the invention is useful for inhibiting TALL-1 conformation a vaccine a vaccine archititis, systemic lupus erythematosus, insulin dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, carave's disease, autoimmune themolytic anaemia, autoimmune thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, autote rheumatic fever, post-streptococcal glomerulonephritis and cutte rheumatic fever, post-streptococcal glomerulonephritis and polyarteritis nodosa. The present sequence represents human BCMA.
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 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 GLSLIISLAVFVLMFILRKISSEPLKDEFKNTGSGIJGMANIDLEKSRTGDEIILFRGLE 120
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 Novel TALL-1 antagonist protein useful for inhibiting TALL- 1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNALLMTCL 60
 1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNALLWTCL
 Gaps
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 100.0%; Score 964; DB 6; Length 184; 100.0%; Pred. No. 9.7e-95; ive 0; Mismatches 0; Indels (
 (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 ABP60552 standard; protein; 184 AA.
 Claim 62; Page 613; 618pp; English
 Human tumour necrosis factor BCMA.
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 2001US-0345106P.
2002US-0348962P.
2002US-0354966P.
 24-OCT-2002; 2002WO-US034376.
 13-AUG-2002; 2002US-0403364P.
 ž
 (first entry)
 Query Match
Best Local Similarity 100.
Marches 184; Conservative
 Liu
 WPI; 2003-403345/38.
 Shu H,
 181 ISAR 184
 ISAR 184
 N-PSDB; ADA49360.
 Sequence 184 AA;
 24-OCT-2001;
 14-JAN-2002;
07-FEB-2002;
 28-MAR-2003
 121
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 ABP60552
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 RESULT 12
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The invention relates to a novel antibody or its fragment, which immunospecifically binds tumour necrosis factor Delta (TNF-delta/APRIL). The antibody of the invention has dermacological, immunosuppressive, antiallergic, antiabedic, antiatric; cytostatic, antianaemic, antiallatic, cytostatic, antianaemic, antiallatic, antianaemic, antiallatic, antiabetic, antiphoriatic, anti-HIV, antianaemic, antiallatic, antiabetic, antiphoriatic, anti-HIV, antiarteriosclerotic, vasotropic, thyromimetic, and preventing or complaination of sease or disorder such as autoimmune disease, and graft versus cythemateous, rheumatoid arthritis or Sjogren's syntem. ParkIL or APRIL receptor expression or aberrant function of APRIL or APRIL receptor expression or aberrant function of APRIL or APRIL ceptor expression or aberrant function of APRIL or APRIL ceptor as autoimmune neutropenia, haemolytic anaemia, dermatitis, asthma, allergic encephalomyellitis, myocarditis, multiple sclerosis, cuveitis, tuberroulosis, diabetes mellitus, psoriasis, cancer of the immune system, particularly B cell cancers, immune disorders such as myasthenia gravis. Hashimoto's disease, immunodeficiency syndrome (AIDSS), and gravis, Hashimoto's disease, immunodeficiency syndrome (AIDSS), and gravis, tumour necrosis factor BCMA.
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 dermatological; immunosuppressive; antiinflammatory; antirheumatic; antiarthritic; cytostatic; antianaemic; antiallergic; antiasthmatic; neuroprotective; ophthalmological; tuberculostatic; antidiabetic; anti-HUY, antiarteriosclerctic; vasotropic; thyromimetic; haemostatic; cancer; autoimmune disease; graft versus host disease; inflammatory disorder; proliferative disorder; single chain antibody; antibody; human; BCMA; tumour necrosis factor.
 9
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 Novel isolated antibody that immunospecifically binds tumor necrosis factor delta, useful for treating, preventing or ameliorating Non-Hodgkin's lymphoma, multiple myeloma, rheumatoid arthritis or Sjogren's
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 YTVEBCTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNALLWTCL
 1 MIQWAGQCSQNEYFDSILHACIPCQLRCSSNTPPLICQRYCNASVINSVKGINAILWTCL
 GLSLIISLAVFVIMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
scFv; immunospecific; tumour necrosis factor delta; TNF-delta;
 Gaps
 0;
 Score 964; DB 6; Length 184; Pred. No. 9.7e-95; O; Mismatches O; Indels C
 Disclosure; Page 222; 225pp; English.
 100.0%;
100.0%;
 22-MAY-2002; 2002WO-US016106.
 24-MAY-2001; 2001US-0293100P.
 (HUMA-) HUMAN GENOME SCI INC.
 Matches 184; Conservative
 WPI; 2003-156740/15.
 Similarity
 Sequence 184 AA;
 WO200294192-A2.
 Homo sapiens
 28-NOV-2002
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 121
 Ruben SM;
 Query Match
Best Local 9
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Sequence 184 AA;
 Homo sapiens.
 15-JAN-2004
 31-JUL-2003
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 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPPAALSATEIEKS 180
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLPRGLE 120
 GLSLIISLAVFVLMFILRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
 The present sequence represents a human BCMA polypeptide. The specification also describes TACI and BR3 polypeptides. TACI and BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April bind to the TACI receptor, while TNF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for preparing a composition for treating systemic lupus erythematosus
 MLÓMAGOCSÓNEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL 60
 BR3; receptor; tumour necrosis factor ligand; TNF ligand;
 121 YTVEECTCEDCIKSKPKVDSDHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 Gaps
 New nucleic acid encoding a TACIs or BR3 polypeptide, useful for preparing a composition for treating systemic lupus erythematosus
 ö
 Length 184;
 100.0%; Score 964; DB 6; Length 10
100.0%; Pred. No. 9.7e-95;
ive 0; Mismatches 0; Indels
 TALL-1; April; systemic lupus erythematosus; BCMA
 of human BCMA receptor.
 Yan
 ABP97717 standard; protein; 184 AA
 Disclosure; Fig 2; 153pp; English.
 Ridgway J,
 24-JUL-2002; 2002WO-US023487.
 03-AUG-2001; 2001US-0310114P.
30-APR-2002; 2002US-0377171P.
 (first entry)
 Matches 184; Conservative
 (GETH) GENENTECH INC.
 Amino acid sequence
 Dixit V, Grewal I,
 WPI; 2003-256560/25.
 Similarity
 ISAR 184
 ISAR 184
 ISAR 184
 ISAR 184
 N-PSDB; ABZ68871
 Sequence 184 AA;
 WO2003014294-A2.
 Homo sapiens
 Human; TACI;
 28-MAY-2003
 20-FEB-2003.
 ABP97717;
 181
 121
 181
 61
 181
 Query Match
 181
 Local
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ABP9771
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The present invention describes an isolated polynuclectide (I), which is overexpressed in haematological malignancies, and which encodes a coverexpressed in haematological malignancies, and which encodes a colypeptide or an immunogenic fragment of the polypeptide. (2) an expression vector comprising (I) operably linked to an expression control sequence; (3) a constraint of the polypeptide or its immunogenic fragment; and specifically binds to the polypeptide or its immunogenic fragment; encoded by (i). (i) has cytostatic and immunostimulant activities, and can be used in vaccines and immunostherapy. The immunoconjugates are useful in composition for treating cancer, e.g. multiple myeloma call, chronic lymphocytic leukaemia, B cell leukaemia, and imultiple myeloma in humans, sheep, primates, goats, bovines, equines, porcines, lupines, cancer agents, and generating antibodies or immunoconjugates for treating cancer. Cancer agents, and generating antibodies or immunoconjugates for treating cancer agents, and generating antibodies or immunoconjugates for treating cancer agents, and generating antibodies or immunoconjugates for treating corporation or mathodogy can be used for detecting, diagnosing or propropried or antibody can be used for detecting, diagnosing or present sequence is used in the exemplification of the present invention.
 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL 60
 haematological malignancy; immunoconjugate; cytostatic; immunostimulant;
 vaccine; immunotherapy; cancer; multiple myeloma cell;
chronic lymphocytic leukaemia; B cell leukaemia; lymphoma; anti-cancer;
 1 MLOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL
 Gaps
 New hematological malignancy-related genes and polypeptides, useful screening anti-cancer agents, and generating antibodies or immunoconjugates for treating e.g. multiple myeloma cell or chronic
 Ordonez N;
 ö
 Length 184;
 Indels
 Wang A,
 100.0%; Score 964; DB 7;
100.0%; Pred. No. 9.7e-95;
ive 0; Mismatches 0;
 Clapper JD,
 Claim 9; SEQ ID NO 4; 307pp; English.
ADD67527 standard; protein; 184 AA
 Human Ly1732P protein SEQ ID NO:4.
 Mannion J,
 22-JAN-2003; 2003WO-US002353.
 22-JAN-2002; 2002US-00057475.
 (first entry
 Conservative
 Gaiger A, Algate PA,
Carter L, Mcneill PD;
 lymphocytic leukemia.
 WPI; 2003-598749/56.
 (CORI-) CORIXA CORP
 Query Match
Best Local Similarity
Matches 184; Conserv
 WO2003062401-A2..
 N-PSDB; ADD67526.
 δ
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GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS

184

entry)

(first

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CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;
Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;
Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;
Antibacterial; antiparasitic; systemic lupus erythematosus;
diabetes mellitus; AIDS; BCMA.
 ADK00756 standard; protein; 184 AA.
 25-JUL-2002; 2002US-0398530P
 25-JUL-2003; 2003WO-US023421
 (GETH) GENENTECH INC.
 Native human BCMA
 181 ISAR 184
 Chuntharapai A,
 WO2004011611-A2
 Homo sapiens.
 06-MAY-2004
 05-FEB-2004
 121
 ADK00756;
 61
 181
 RESULT 16
 ADK00756
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 method of the invention has neuroprotective, nootropic, and antiinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative
 The invention relates to a novel method for treating a neurodegenerative immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA ligand (the mammal has or is at risk of developing multiple sclerosis). The
 , neurodegenerative immunological disorder; demyelination; al Nervous System; CNS; inflammation; B-cell maturation antigen; multiple sclerosis; neuroprotective; nootropic; antiinflammatory;
 Treating a neurodegenerative immunological disorder, e.g. demyelination or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
 immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence represents human BCMA.
121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 100.0%; Score 964; DB 7; Length 184; 100.0%; Pred. No. 9.7e-95; ive 0; Mismatches 0; Indels
 Human B-cell maturation antigen SEQ ID NO:1.
 ADG43715 standard; protein; 184 AA.
 Claim 8; Page 68-69; 72pp; English.
 21-FEB-2003; 2003WO-US005147.
 21-FEB-2002; 2002US-0358427P
 WPI; 2003-721758/68.
N-PSDB; ADG43716.
 Reid H;
 (BIOJ) BIOGEN INC.
 Similarity
 ISAR 184
 ISAR 184
 Central Nervous
 Sequence 184 AA;
 WO2003072713-A2
 Homo sapiens.
 BCMA, multipl
gene therapy.
 26-FEB-2004
 Kalled SL,
 ADG43715;
 61
 121
 181
 Query Match
 human;
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Kim KJ,

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Grewal

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The present invention relates to an isolated monoclonal antibody which binds to a transmembrane activator of and CAML interactor (TACI) receptor. The TACI antibodies are useful for modulating TALL-1 or TACI polypeptide biological activity in mammalian cells, or for diagnosing and treating pathological conditions associated with TNF and TNF receptor-related molecules, e.g. cancer or immune-related disease, such as systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome, systemic vasculitis, diabetes mellitus, Crohn's disease, glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or infection, fungal infection, hepresent sequence represents native human BCMA.
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 useful for diagnosing and with tumor necrosis factor, as rheumatoid arthritis or
 MIQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 1 MLQMAGQCSQNBYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 ;
0
 100.0%; Score 964; DB 8; Length 184; 100.0%; Pred. No. 9.7e-95; ive 0; Mismatches 0; Indels (
 New anti-TACI receptor monoclonal antibody, treating pathological conditions associated e.g. cancer or immune-related disease, such
 Disclosure; SEQ ID NO 6; 110pp; English
 Conservative
WPI; 2004-143841/14.
N-PSDB; ADK00755.
 Similarity
 Sequence 184 AA;
 Best Local Simi
Matches 184;
 Query Match
Best Local 8
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Gaps

; 0

GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120

61

1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL 60

1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL

Best Local Similarity luv. Matches 184; Conservative

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ABG95060
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 The present invention relates to the use of an agonist or antagonist of Genoxit activity for preventing or treating obesity. Genoxit is a member of the Tumour Necrosis Factor Receptor Super Family and is a Type III transmembrane protein. The agonists or antagonists of the invention are useful for treating or preventing obesity-related diseases or disorders, e.g. obesity, insulin resistance, atherosclerosis, atheromatous disease, heart disease, e.g. cardiac insulficiency, coronary insufficiency, high blood pressure), hypertension, stroke, syndrome X, diabetes mellitus (type I and II), hyperlipidaemia and hyperuricaemia, also diabetic
 genoxit; anorectic; antilipaemic; antiarteriosclerotic; cardiant;
 New use of agonist or antagonist of Genoxit activity for preventing or treating obesity-related diseases or disorders, e.g. hyperlipidemia and atherosclerosis.
 atheromatous disease; heart disease; hypertension; stroke; syndrome X; diabetes mellitus; hyperlipidaemia; hyperuricaemia.
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 YTVEECTCEDCIKSKPKVDSDHCPPLPAMBEGATILVTTKTNDYCKSLPAALSATEIEKS
 antidiabetic; hypotensive; ophthalmological; neuroprotective; nephrotropic; obesity; Tumour Necrosis Factor Receptor Super Family; Type III transmembrane protein; insulin resistance; atherosclerosis;
 1. .54
/label= Extracellular domain
 5. .77
label= Transmembrane domain
 78. .184
/label= Intracellular_domain
 Location/Qualifiers
 Disclosure, Page 32; 35pp; English.
 ABR40082 standard; protein; 184 AA
 label= Gln, Lys
 Briggs K;
 05-AUG-2002; 2002WO-IB003498
 06-AUG-2001; 2001US-0310754P
 (first entry)
 Lucas J, Dialynas D,
 2003-268160/26.
 ISAR 184
 isak 184
 N-PSDB; ACC00340.
 Misc-difference
 WO2003013582-A1
 (GEST) GENSET
 sapiens
 27-JUN-2003
 20-FEB-2003
 ABR40082;
 61
 121
 121
 181
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 Domain
 Domain
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ABR40082
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 The invention describes a method of treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins (I), treating cancerous cells containing (I) in a heterogeneous cell population, treating proliferative diseases associated with mutant protein or cellular protein isoforms (II) dependent on heat shock protein
 9
 9
 Treating genetically-defined disease associated with chromosomal aberrations yielding oncogenic fusion proteins, e.g. cell proliferative diseases, involves administering an inhibitor of heat shock protein 90.
 protein 90;
 1 MLXWAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLPRGLE
 121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS
 121 YIVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKINDYCKSLPAALSATEIEKS
 1 MLQMAGQCSQNBYPDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 Gaps
 CMML;
 Chromosome aberration; oncogenic fusion protein; cancer; proliferative disease; cellular protein isoform; heat shock protein isoform; heat shock protein isoform; heat shock protein; if the match arthritis; cancer; haematopoietic disorder; a cell lymphona; B cell lymphona; chronic myeloid leukaemia; CMU; acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML; acute lymphoblastic leukaemia; ALL; APL; MLI; solid tumour; papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma; rhabdomyosarcoma; synovial sarcoma; viral infection.
 ..
complications, e.g. microangiopathic lesions, ocular lesions, retinopathy, neuropathy and renal lesions
 Length 184;
 1; Indels
 Score 958; DB 6;
Pred. No. 4.3e-94;
 Human translocation (4; 16) (q26; p13) protein.
 Score 958; DB
 Mismatches
 Disclosure; Page 189-190; 389pp; English
 Ą
 (CONF-) CONFORMA THERAPEUTICS CORP.
 ö
 ABG95060 standard; protein; 288
 99.4%;
 01-MAR-2002; 2002WO-US006518.
 01-MAR-2001; 2001US-0272751P.
 04-DEC-2002 (first entry)
 Matches 183; Conservative
 Fritz LC, Burrows FJ;
 2002-698710/75.
 Similarity
 184
 181 ISAR 184
 N-PSDB; ABS73235
 Sequence 184 AA;
 WO200269900-A2.
 ISAR
 12-SEP-2002,
 ABG95060;
 181
 Query Match
Best Local
 Homo
 RESULT 18
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definistering HSP90-inhibitor. The method is useful for treating administering HSP90-inhibitor. The method is useful for treating genetically-defined disease with chromosomal aberration yielding oncogenic fusion protein, treating cancerous cells containing fusion protein, treating cancerous cells containing fusion protein in heterogeneous cell population, treating proliferative disease (e.g. rheumatoid arthritis or cancer) associated with mutant protein or cellular protein isoform dependent on heat shock protein for cellular protein isoform in a patient heteroxygous for (II). The method is useful for treating a disease e.g. haematopoietic disorder such as T or B cell imphoma, chronic myeloid leukaenia (CML), APL, ALL, AML, NHL and CMML, or a disease characterised by a solid tumour such as papillary thyroid or a disease characterised by a solid tumour such as papillary thyroid carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and synovial sarcoma. The method is also useful for treating viral infections. This represents a protein encoded by the DNA sequence of a
 Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; Pymphoproliferatined; pancreatic; prostate; tinflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; colon's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis:
 5. .38
Anote "Cysteine-rich consensus region; This is region is specifically claimed as SBQ ID NO: 7 in claim 1 of the specification"
 106 LKMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLG 165
 166 LSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEY 225
 226 TVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATBIEKSI 285
 LSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEY 121
 TVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSI 181
 2 LOMAGOCSONEYFDSLLHACIPCOLKCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLG
 0; Gaps
 Score 955; DB 5; Length 288; Pred. No. 1.6e-93; 1; Mismatches 0; Indels
 /label= Transmembrane_domain
 Human B-cell maturation (BCMA) protein.
 Location/Qualifiers
 AAE15484 standard; protein; 181 AA
 99.1%;
99.5%;
 (first entry)
 Best Local Similarity 99.5
Matches 182; Conservative
 chromosome aberration
 Sequence 288 AA;
 SAR 184
 SAR 288
 WO200187979-A2
 Homo sapiens.
 22-NOV-2001.
 12-MAR-2002
 AAE15484;
 62
 122
 182
 Query Match
 Region
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI BCMA, or the TACI/CC EdMily ligand), having the consensus sequence, but not the extracellular region of TACI or BCMA in a mammal which is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell and/or BCMA in a mammal which is useful for treating B-cell or T-cell and/or BCMA in a mammal which is useful for treating and the mour. APRIL BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriaals, allergies, pneumonia, aropic dermatitis, respiratory allergic disease (asschma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (CIChM's disease, collitis), solleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systems (HIV), atherosclerosis, cancer it heurocycle infiltration of the skin or organs. The present sequence
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
 124 BECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
 9
 LISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTV
 1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVINSVKGTNAILMTCLGLS
 4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
 Human BAFF receptor (BAFF-R) sequence encoded by A plasmid pJST535.
 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent;
 98.5%; Score 950; DB 5; Length 181; 100.0%; Pred. No. 3e-93;
 0; Indels
 100.0%; Prec. ...
 Disclosure; Fig 10A; 94pp; English.
 AAB60700 standard; protein; 157 AA
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
14-MAY-2001; 2001WO-US015567.
 22-MAY-2001 (first entry)
 Query Match
Best Local Similarity 100.1
Matches 181; Conservative
 is human BCMA protein
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
 Yu G;
 Sequence 181 AA;
 184 R 184
 rheill LE,
 AAB60700;
 121
 181
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 RESULT 20
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lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
immune-related disorder; B-cell growth inhibitor; BCMA;
B-cell maturation inhibitor; immunoglobulin production inhibitor;
autoimmune disorder; B-cell lymphoproliferative disorder; hypertension;
renal disorder; immunosuppressive disorder; HIV infection;
 organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; plasmid pdSF535.
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell
 Schneider P;
 Tschopp J,
 Browning J, Ambrose C,
 Sxample 1; Fig 3; 59pp; English.
 16-AUG-2000; 2000WO-US022507.
 11-FEB-2000; 2000US-0181684P.
 (BIOJ) BIOGEN INC.
(APOT-) APOTECH R & D SA.
 WPI; 2001-202866/20.
 N-PSDB; AAF60000
 40200112812-A2
 Homo sapiens
 17-AUG-1999;
 22-FEB-2001
 Thompson J;
 Mackay F,
```

The invention relates to the use of a BAFF receptor (BAFF-R, also known as BCMA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TNF (tumour necrosis factor) [anally, acting as an immunoregulatory capent, and also plays a role in the development of hypertension and capent, and also plays a role in the development of hypertension and percent of secondaring it, and BAFF-R. specific antibodies can be used for inhibiting B-cell growth, dendritic call-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autonomy and immunoglobulin production, and in the treatment of immunosuppressive disorders and HIV closed in the treatment of immunosuppressive disorders and HIV closed in the treatment of immunosuppressive disorders and HIV corteins or BAFF-R specific antibodies may be used for treating, between BAFF-R and BAFF-R thereby inhibiting inflammation. Since BAFF-R inhibits B-cell growth and maturation it is useful for treating diseases such as systemic lupus erythmatosus, autoimmune haemolytic anaemia, grave's disease, multiple myeloma, B-cell carcinomas, lumphomas, lumphomas, lumphomas, lumphomas, lumphomas, lumphomas, lumphommune disorders and inherited B-cell associated disorders and inherited B-cell associated disorders. The bare in the language of the BAFF in the signification in the significance of the ģ PJST535. However, this BAFF-R protein sequence is 27 amino acids than that given in AAB60698 present sequence represents a human BAFF-R protein sequence as encoded plasmid DJST535. However, this BAFF-R protein sequence is 27 amino acid

Sequence 157 AA;

MIQMAGOCSONEYFDSILHACIPCOLRCSNTPPLICORYCNASVTNSVKGTNAILWTCL 60 Gaps Query Match 74.6%; Score 719.5; DB 4; Length 157; Best Local Similarity 85.3%; Pred. No. 1.2e-68; Matches 157; Conservative 0; Mismatches 0; Indels 27.

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YTVEBCTCEDCIKSKPKVDSDHCPPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180 153 GLSLIIS----FVLMFLLRKISSEPLKD----NTGSGLLGMANIDLEKS----DEIILPRGLE ISAR 157 **ISAR** 184 52 121 181 154 RESULT 21 AAB08844 g 윱 Š 셤 Š

AAB08844 standard; peptide; 185 AA. (first entry) 02-JAN-2001 AAB08844; 

BCMA; necrosis factor-kB activator; NF-kB; gene expression; cancer; anti-cell death gene; apoptosis; viral infection; inflammatory response; rheumatoid arthritis; inflammatory bowel disease; septic shock. Amino acid sequence of murine BCMA polypeptide.

Mus musculus

/note= "putative transmembrane domain" Location/Qualifiers Domain

WO200050633-A1

31-AUG-2000

24-FEB-2000; 2000WO-US004925.

99US-0121485P. 24-FEB-1999;

(GEHO ) GEN HOSPITAL CORP.

Seed B, Ting A;

WPI; 2000-558405/51.

death Identifying a modulator of gene expression for drug designing, by contacting a compound library with a cell expressing an anti-cell degene and reporter gene, and determining alteration in reporter gene expression

Claim 32; Fig 7B; 53pp; English.

a necrosis factor (NP)-kB activator. The method of the invention is used activity, compounds which modulate BCMA activity (and thus NP-kB activity). The specification describes a method of identifying a polypeptide which increases gene expression from a promoter. The method involves contacting a library of with a cell which expresses the ecombinant anti-cell death gene and a reporter gene operably linked to the promoter, and then determining whether the expression of the reporter gene is altered as a result of contact with library. The method is useful for identifying polypeptides which increase or decrease gene expression from a promoter. The BCMA polypeptide or nucleic acid are useful for preparing a pharmaceutical composition for treating cancer, apoptosis, viral infections, inflammatory response, such as rheumatoid arthritis, inflammatory bowel disease or septic shock. BCMA is useful for identifying compounds that modulate NF-kB expression and thus for drug The present sequence represents a BCMA (not defined) designing

Sequence 185 AA;

Score 572; DB 3; Length 185; Pred. No. 9.6e-53; 59.3%; 62.6%; Best Local Similarity Query Match

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The present invention relates to Tumour necrosis factor (TNF) and Apolrelated Leucocyte expressed Ligand 1 (TALL-1) nucleic acid molecules, proteins (including homologues), and their antibodies. The invention in particular relates to methods for requlating the interaction between TALL-1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to regulate monocyte, macrophage and B lymphocyte mediated immune responses. TALL-1 protein is useful for identifying compounds that regulate B lymphocyte proliferation. It is also useful for treating B lymphocyte associated autoimmune disorders like rhemmatoid arthritis, systemic lupus erythematosus (SLE), insulin dependent diabetes mellitus, multiple sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1; therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus; SIE; insulin dependent diabetes mellitus; thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome; haemolytic anaemia; Grave's disease; myasthenia gravis; BCWA; call maturation factor; pemphigus vulgaris; B-lymphocyte proliferation; post-streptococcal glomerulonephritis; polyarteritis nodosa.
 63
 m
 MAGQCSQNEYPDSLLHACI PCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
 LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL
 Gaps
 Isolated TALL-1 protein is used to identify compounds that regulate lymphocyte proliferation, used to treat B lymphocyte associated autoimmune disorders.
 8
 Murine; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
21; Mismatches 41; Indels
 Murine B cell maturation factor (BCMA) protein.
 Claim 37; Page 107-108; 112pp; English.
 (NAJE-) NAT JEWISH MEDICAL & RES CENT,
 AAY71980 standard, protein, 185 AA
 06-MAY-1999; 99US-0132892P.
 05-MAY-2000; 2000WO-US012266.
 (first entry)
117; Conservative
 EKSISAR 184
 EKPTHTR 185
 WPI; 2001-016094/02.
 N-PSDB; AAD02130.
 WO200068378-A1
 Mus musculus.
 28-MAR-2001
 16-NOV-2000
 59
 120
 119
 178
 179
 Shu HS;
Matches
 AAY 11980

AAY 71980

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AAC

AAY 7

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AAY 7

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BAY 9

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pemphigus vulgaris, acute rhematic fever, post-streptococcal glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its corresponding mucleic acid sequence are also useful in diagnostic assays. The present sequence is a murine B cell maturation factor (BCMA). BCMA is the receptor for TALL-1 protein
 119
 Mouse; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psortasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 120 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 28
 1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLMIFLGLT
 4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
 LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL
autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
 ..
 41; Indels
 Match 59.3%; Score 572; DB 4; Local Similarity 62.6%; Pred. No. 9.6e-53; Les 117; Conservative 21; Mismatches 41;
 Mouse B cell maturation (BCMA) protein.
 rheumatoid arthritis; atherosclerosis.
 AAE15490 standard; protein; 185 AA.
 Disclosure, Fig 11, 94pp; English
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567
 (first entry)
 EKPTHTR 185
 EKSISAR 184
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
 Yu G;
 Sequence 185 AA;
 WO200187979-A2
 12-MAR-2002
 22-NOV-2001
 Theill LE,
 64
 119
 178
 AAE15490;
 Query Match
 Mus sp
 ligand
 AAE15490
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14-MAY-2001; 2001US-00214591.

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF ETMIL) ligand), having the consensus region of TACI BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell symphoproliferative discorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function
 BYTVEECTCEDCVKSKPKGDSDHFFPLPAMEGATILVTTKTGDYGKSSVPTALQSVMGM·178
 cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriaeis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;
 64 LIISLAVFVIMFILIRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
 diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
 120 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
 1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
 4 MAGQCSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
 transmembrane activator and intracellular CAML interactor; TACI;
 Gaps
 Human B cell maturation protein cysteine rich extracellular region.
 59.3%; Score 572; DB 5; Length 185; 62.6%; Pred. No. 9.6e-53; ive 21; Mismatches 41; Indels
 rheumatoid arthritis; atherosclerosis
 AAE15501 standard; peptide; 58 AA
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
 14-MAY-2001; 2001WO-US015567
 (first entry)
 Best Local Similarity 62.6
Matches 117; Conservative
 mouse BCMA protein
 EKSISAR 184
 EKPTHTR 185
 Sequence 185 AA;
 WO200187979-A2.
 Homo sapiens
 12-MAR-2002
 22-NOV-2001.
 AAE15501;
 59
 119
 Query Match
 178
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, capatrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antegonists are useful for treating inflammacion and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic carmatitis, respiratory allergic disease (asthma, hypersensitivity) lung disease), drug and insect sting allergy, inflammatory bowel disease (crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumaciod arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA cysteine-rich extracellular region
 ö
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; cohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; mouse.
 8 CSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLI 65
 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLI 58
 Gaps
 Human-murine B cell maturation protein (BCMA) consensus sequence.
 ö
 33.5%; Score 323; DB 5; Length 58; 100.0%; Pred. No. 9.9e-27; Live 0; Mismatches 0; Indels
 AAE15491 standard; protein; 117 AA
 Disclosure; Fig 13; 94pp; English.
 (first entry)
 Conservative
 (revised)
 WPI; 2002-066686/09
 Local Similarity
 (AMGE-) AMGEN INC.
 Sequence 58 AA;
 WO200187979-A2
 Homo sapiens
 29-AUG-2003
12-MAR-2002
 58;
 22-NOV-2001
 rheill LE,
 Mus sp.
Chimeric.
 AAE15491;
 Query Match
 Matches
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B-cell maturation inhibitor; immunoglobulin production inhibitor;
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 The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (970, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA attracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, actopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, collitis), soleroderma, autoinamne disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucoyce infiltration of the Skin or organs. The present sequence is human-murine B cell maturation protein (BCMA) consensus sequence. (Updated on 29-AUG-2003 to standardise OS field)
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 69 AVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLPRGLEYTVEECTC 128
 9 SQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISL 68
 43
 44 A----FFLLRK----ELKDE-----GSLAL------RGD---IPR-LEYTVEECTC 76
 Mouse IgG signal/human BAFF-R/human IgG Fc fusion protein, BAFF-R-Fc.
 Human BAFF-R; BAFF receptor; TNF family; immunoregulatory agent; immune-related disorder; B-cell growth inhibitor;
 49;
 32.3%; Score 311.5; DB 5; Length 117; 61.5%; Pred. No. 4.2e-25; ive 4; Mismatches 7; Indels 49;
 129 EDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDY 164
 EDC-KSKPK-DSDH-FPLPAMEEGATILVTTKT-DY 108
 Disclosure; Fig 11; 94pp; English.
 AAB60699 standard; protein; 302
 14-MAY-2001; 2001WO-US015567.
 2000US-0204039P.
 27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 (first entry)
 Local Similarity 61.5
les 96; Conservative
 (revised)
 WPI; 2002-066686/09
 Theill LE, Yu G;
 (AMGE-) AMGEN INC
 Sequence 117 AA;
 12-MAY-2000;
 11-SEP-2003
22-MAY-2001
 AAB60699;
 Query Match
 77
 ligand.
 Best Loc
Matches
 RESULT 26
 AAB60699
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The invention relates to the use of a BAFF receptor (BAFF-R, also known as BORA) protein, or a BAFF-R fusion protein as an agent for the treatment of a variety of immune-related disorders. BAFF-R is a member of the TMF (tumour necrosis factor) family, acting as an immunoregulatory agent, and also plays a role in the development of hypertension and related disorders. BAFF-R, fusion proteins containing it, and BAFF-R. specific antibodies can be used for inhibiting B-cell growth, dendritic cell-induced B-cell growth and maturation, and immunoglobulin production, and in the treatment of autoinmune disorders. The BAFF-R proteins may also be used in the treatment of immunosuppressive disorders and HIV infection, and in patients undergoing organ transplantation. The BAFF-R proteins or BAFF-R specific antibodies may be used for treating, suppressing or altering an immune response involving a signalling pathway suppressing or altering an immune response involving a signalling pathway inhibits B-cell growth and maturation if is useful for treating diseases inthibits B-cell growth and maturation in law in systemic lupus erythematosus, autoimmune haemolytic aniaemia.
 Inhibiting dendritic cell-induced B-cell growth, maturation and B-cell lympho-proliferative disorder by administering BAFF-receptor polypeptide, chimeric molecule comprising receptor or anti-BAFF-R antibody homolog.
 Grave's disease, multiple myeloma, B-cell carcinomas, leukaemia, rapidly progressive glomerulonephritis, and lymphomas. Nucleic acids encoding human BAFF-R may be used in gene therapy to treat tumours, lymphomas, autoimmune disorders and inherited B-cell-associated disorders. The
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autoimmune disorder; B-cell lymphoproliferative disorder; hypertension; renal disorder; immunosuppressive disorder; HIV infection; organ transplantation; antiinflammatory; systemic lupus erythematosus; autoimmune haemolytic anaemia; Grave's disease; multiple myeloma; B-cell carcinoma; leukaemia; rapidly progressive glomerulonephritis; lymphoma; gene therapy; cancer; tumour; IgG Fc; fusion construct.
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 24 MLOWAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGVDK-THTC-
 present sequence represents the BAFF-R fusion protein BAFF-R-Fc, comprising a mouse IgG-kappa signal sequence, residues 1-153 of human
 a mouse IgG-kappa signal sequence, residues 1-153 of a human IgG Fc sequence. (Updated on 11-SEP-2003 to
 Length 302;
 Browning J, Ambrose C, Tschopp J, Schneider P;
 Indels
 DB 4;
 29.7%; Score 286.5; DB 4;
39.9%; Pred. No. 7e-22;
iive 13; Mismatches 54;
 Example 4; Fig 2; 59pp; English
 16-AUG-2000; 2000WO-US022507.
 11-FEB-2000; 2000US-0181684P.
 99US-0149378P.
 (APOT-) APOTECH R & D SA.
 Conservative
 standardise OS field)
 2001-202866/20.
 (BIOJ) BIOGEN INC.
 Similarity
 N-PSDB; AAF59999
 Sequence 302 AA;
 WO200112812-A2.
 17-AUG-1999;
 Homo sapiens
 81;
 22-FEB-2001
 Thompson J;
 comprising
BAFF-R and
 Mackay F,
 Chimeric.
 Query Match
Best Local 8
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Chimeric.
Homo sapiens.
 ADG43717;
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 PAPELLGGPSVFLFPPKPKDTLMISRTPE 113
 114 VI---CVVVDVSHEDPEVKFNWYVDGVBVHNAKIKPREEQYNSTYRVVSVLIVLHQDWLN 170
 Treating a mammal for a condition associated with undesired cell proliferation such as cancer or carcinoma, comprises administering a composition comprising A Proliferation Inducing Ligand Receptor (APRIL-R)
 Human; A Proliferation Inducing Ligand Receptor; APRIL-R; cytostatic; gene therapy; cancer; nephrotropic; renal disorder; autoimmune disease; carcinoma; lung; colon; breast; prostate; Grave's disease; hypertension; systemic lupus erythematosus; SLE; inflammation; cardiovascular disease;
 B-cell lympho-proliferative disorder; BCM; immunosuppressive disease; organ transplantation; HIV; human immunodeficiency virus; TNF; murine; tumour necrosis factor; B cell maturation protein; BCMA; fusion protein; immunoglobulin G; IgG; Fc region.
GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 YTVEECTCEDCIKSKPKVDSD-----HCPPLPAMEE-----GATILVTTKTNDY--
 /label= Mature_human_BCMA_IgG_Fc_fusion_protein
 1. .22
/label= Signal peptide
/note= "Derived from murine Ig kappa sequence"
 Rennert P;
 76. .302
/note= "Derived from human IgG Fc region"
 "Derived from human BCMA protein"
 Human BCMA-Immunoglobulin G Fc region fusion construct.
 Cachero T, Ambrose C,
 /label= Cysteine rich domain
/note= "Derived From human BCMA"
 171 GKEYKCKVSNKALPA-PIEKTIS 192
 ----CKSLPAALSATEIEKSIS 182
 Location/Qualifiers
 AAE00507 standard; protein; 302 AA.
 11-FEB-2000; 2000US-0181807P.
 99US-0157933P.
 05-OCT-2000; 2000WO-US027579
 (first entry)
 Schneider P, Thompson J,
 .302
 (APOT-) APOTECH R & D SA.
 23. .75
 'note=
 (revised)
 2001-266242/27.
 (BIOJ) BIOGEN INC.
 N-PSDB; AAD03847
 WO200124811-A1
 Homo sapiens.
 06-OCT-1999;
 11-SEP-2003
 31-JUL-2001
 12-APR-2001
 antagonist.
 AAE00507;
 Mus sp. .
Chimeric.
 82
 121
 165
 Protein
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The inversion traces to a mention of clearing as manimal total as condition.

The method involves administering a composition comprising A Proliferation inducing Ligand Receptor (APRIL-) also referred as B cell maturation protein (BCM or BCMA) antagonist that antagonises the maturation protein (BCM or BCMA) antagonist that antagonises the interaction between APRIL and its cognate receptor(s). This method is cusful for treating undesired cell proliferation such as cancer or carcinoma, and other carcinoma, colon carcinoma, breast carcinoma, prostate carcinoma, and other carcinomas whose proliferation is modulated by APRIL. It is also useful for treating autolimmune diseases (Grave's disease, renal disorders, B-cell lympho-proliferative disorders, and immunedaticiency virus (HIV), and for treating, suppressing or altering immunodeficiency virus (HIV), and for treating, suppressing or altering a fusion construct containing human APRIL-R also referred as BCMA or BCM protein, For region of human immunoglobulin (1gG) and a signal a signal construct containing human APRIL-R also referred as BCMA or BCM protein, For region of human immunoglobulin (1gG) and a signal
 120
 121 YTVEECTCEDCIKSKPKVDSD------HCFPLPAMEE-----GATILVTTKTNDY-- 164
 114 VI---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 170
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 Central Nervous System; CNS; inflammation; B-ceil maturation antigen; BCMA; multiple sclerosis; neuroprotective; nootropic; antinflammatory;
 The invention relates to a method of treating a mammal for a condition
 24 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGVDK-THTC-
 61 GLSLIISLAVFVLMFLLRKISSEPLKDEPKNTGSGLLGMANIDLEKSRTGDEIILPRGLE
 82 ------PAPELLGGPSVFLFPPKPKDTLMISRTPE
 1 MLOMAGOCSONEYFDSILHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCL
 55;
 human; neurodegenerative immunological disorder; demyelination;
 ; Score 286.5; DB 4; Length 302;
; Pred. No: 7e-22;
13; Mismatches 54; Indels 55;
 note= "Murine IgGkappa signal sequence"
 24. .74
/note= "Human BCMA extracellular domain"
 75. .302
/note= "Human Ig heavy chain Fc region"
 Human B-cell maturation antigen-Fc SEQ ID NO:3.
 165 ----CKSLPAALSATEIEKSIS 182
 171 GKEYKCKVSNKALPA-PIEKTIS 192
 Location/Qualifiers
 ADG43717 standard; protein; 302 AA.
Example 1; Fig 3B; 85pp; English.
 39.98;
 Query Match
Best Local Similarity 35....
Best Cocal 81; Conservative 1
 26-FEB-2004 (first entry)
 standardise OS field)
 gene therapy; mouse.
 Sequence 302 AA;
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 method of the invention has neuroprotective, nootropic, and antiinflammatory activity, and may have a use in gene therapy. The methods, BCMA, and antibodies are useful for treating a neurodegenerative immunological disorder such as multiple sclerosis, demyelination or CNS inflammation. The present sequence is used in the exemplification of the
 Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;
 61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLE 120
 114 VT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 170
 121 YTVEECTCEDCIKSKPKVDSD-----HCFPLPAMEE-----GATILVTTKTNDY-- 164
 The invention relates to a novel method for treating a neurodegenerative
 81
 immunological disorder, demyelination or Central Nervous System (CNS) inflammation in a mammal. The method comprises administering B-cell maturation antigen (BCMA), or an antibody against BCMA or a BCMA (the mammal has or is at risk of developing multiple sclerosis). The
 Treating a neurodegenerative immunological disorder, e.g. demyelination or inflammation in a mammal comprises administering a B-cell maturation antigen (BCMA), an antibody against BCMA or a BCMA ligand.
 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
 24 MLOMAGOCSONEYFDSLIHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGVDK-THTC-
 DB 7; Length 302;
 Indels
 BCMA-immunoglobulin Fc region fusion protein.
 54;
 29.7%; Score 286.5; DB 39.9%; Pred. No. 7e-22; ive 13; Mismatches
 171 GKEYKCKVSNKALPA-PIEKTIS 192
 ----CKSLPAALSATEIEKSIS 182
 Claim 12; Page 70-71; 72pp; English
 AAE15488 standard; protein; 283 AA
 21-FEB-2003; 2003WO-US005147.
 21-FEB-2002; 2002US-0358427P
 (first entry)
 Local Similarity 39.9
Les 81; Conservative
 WPI; 2003-721758/68.
N-PSDB; ADG43718.
 Kalled SL, Reid H;
 (BIOJ) BIOGEN INC.
 Sequence 302 AA;
 WO2003072713-A2
 12-MAR-2002
 04-SEP-2003
 82
 AAE15488;
 165
 Query Match
 Human
 Matches
 AAE15488
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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (GTO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/ BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI or DATA. The mammal which is useful for inhibiting activity of TACI or DATA. The mammal which is useful for inhibiting activity of TACI or DATA. The mammal which is useful for inhibiting activity of TACI or BCMA in a mammal which is useful for inhibiting activity of TACI or DATA. The macroal conformation is such as lung gastrointesitual, pancreatic or prostate tumour. ARRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis, soleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein-immunoglobulin Fc region fusion protein
 64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSG-------LLGMANIDLEKSRTG 110
 activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 111 DEIILPRGLEYTVEECTCEDCIKSKPKVDSD-----HCFPLPAMEE-----GATIL 156
 85 DILMISRIPEVI---CVVVDVSHEDPEVKENWYVDGVEVHNAKIKPREEQYNSIYRVVSV 141
 51
 84
human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein.
 ------GGGGGDKTHTCPPCPAPELLGGPSVFLFPPKPK
 Inhibiting activity of B cell maturation protein and/or transmembrane
 4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
 1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA-----
 74;
 Length 283;
 47; Indels
 ; Score 286; DB 5;
; Pred. No. 7.3e-22;
12; Mismatches 47;
 157 VITKTNDY-----CKSLPAALSATEIEKSIS 182
 142 LIVLHQDWLNGKEYKCKVSNKALPA-PIEKTIS 173
 Disclosure; Fig 10B; 94pp; English.
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 29.7%;
37.6%;
 14-MAY-2001; 2001WO-US015567.
 Conservative
 WPI; 2002-066686/09.
 Similarity
 (AMGE-) AMGEN INC.
 Yu G;
 Sequence 283 AA;
 WO200187979-A2
 Query Match
Best Local Simil
Matches 80; C
 22-NOV-2001
 Theill LE,
 52
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AAE15485 standard; peptide; 51 AA
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AAE15485;

(first entry) 12-MAR-2002

Human B-cell maturation (BCMA) protein extracellular domain.

cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis. activator and intracellular CAML interactor; transmembrane

Homo sapiens.

WO200187979-A2

22-NOV-2001.

14-MAY-2001; 2001WO-US015567.

12-MAY-2000; 2000US-0204039P. 27-JUN-2000; 2000US-0214591P. 14-MAY-2001; 2001US-00214591.

(AMGE-) AMGEN INC.

WPI; 2002-066686/09.

Yu G;

Theill LE,

Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family

Claim 1; Fig 10A; 94pp; English.

ligand.

The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRIL (G70, a tumour necrosis factor-TMF family ligand), having the consensus region of TACI, BCMA, or the TACI/ EGMA to the TACI and/or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA. The method is useful for treating B-cell or T-cell impoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic demactitis, respiratory allergic disease (asthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atheroseclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence is human BCMA protein extracellular domain 

Sequence 51 AA;

0 Gaps ö 29.5%; Score 284; DB 5; Length 51; 100.0%; Pred. No. 1.3e-22; 0; Indels 100.0%; Pred. A.C. Query Match
Best Local Similarity 100.
Matches 51, Conservative

4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA 54 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA 51

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AAE15486 ID AAE1

AAE15486 standard; peptide; 34 AA

AAE15486;

(first entry) 12-MAR-2002 Human B-cell maturation (BCMA) protein cysteine-rich consensus region.

Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; crobm's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis

Homo sapiens

WO200187979-A2.

22-NOV-2001.

14-MAY-2001; 2001WO-US015567

12-MAY-2000; 2000US-0204039P.

27-JUN-2000; 2000US-0214591P.

(AMGE-) AMGEN INC.

Yu G; Theill LE, WPI; 2002-066686/09.

Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand

Claim 1; Fig 10A; 94pp; English.

The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering a specific binding partner for APRLI (GTO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in amammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, alergies, puncumonia, atopic diseases und as diarrhoea, psoriasis, alergies, puncumonia, atopic disease, drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer sequence or such an experience or sequence or solver sequence or such and sease to sequence or such and is human BCMA protein cysteine-rich consensus region

Sequence 34 AA;

Gарв ö Length 34; Indels 20.9%; Score 201; DB 5; I 100.0%; Pred. No. 5.7e-14; iive 0; Mismatches 0; Conservative Similarity Ma. Local Si... " Query Match Matches

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41 1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC œ

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The invention relates to a novel TALL-1 antagonist protein, comprising a sequence that differs from SEQ ID NO:2, or amino acids 134-285 of SEQ ID NO:2, by at least one modification in the region connecting &bgr; strands D and E that reduces the biological activity of the TALL-1 antagonist as compared to wild-type TALL-1. A protein of the invention has immunosuppressive, antirheumatic, antinflammatory, antiarthritic, nephrotropic, and vasotropic activity, a TALL-1 antagonist may be used in a vaccine. A protein of the invention is useful for inhibiting TALL-1 biological activity in a mammal. To is useful for inhibiting TALL-1 biological activity in a mammal. To is useful for inhibiting TALL-1 biological activity in a mammal. To is useful for inhibiting TALL-1 biological activity in a mammal. To is useful for inhibiting TALL-1 cases as theumatoid architis, sultiple sclerosis, myasthaenia gravis, dependent diabetes mellitus, multiple sclerosis, myasthaenia gravis, thrombocytopenic purpura, Goodpasture's syndrome, pemphigus vulgaris, cutte rheumatic fever, post-streptococcal glomerulonephritis and polyareritis and present sequence represents a cysteine rich
 Novel TALL-1 antagonist protein useful for inhibiting TALL-1 biological activity in mammal, has a modification in the region connecting beta strands D and E that reduces the biological activity of TALL-1
 TALL-1; antagonist; immunosuppressive; antirheumatic; antinflammatory; antiarthritic; dermatological; antidiabetic; neuroprotective; antiatryroid; antipyretic; nephrotropic; vasciros; vasciros; autoimmune disease; rheumatoid arthriti; systemic lupus erythematosus; insulin dependent diabetes mellitus; multiple sclerosis; myasthaenia gravis; Grave's disease; autoimmune hemolytic anaemia; autoimmune thrombocytopenic purpura; Goodpasture's syndrome; poemphigaris; acute rheumatic fever; post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA; CRD; cysteine rich domain.
 20.9%; Score 201; DB 6; Length 34; 100.0%; Pred. No. 5.7e-14; ive 0; Mismatches 0; Indels
 (NAJE-) NAT JEWISH MEDICAL & RES CENT.
 Disclosure; Page 616; 618pp; English.
 module of human BCMA.
 ADA49366 standard; peptide; 34 AA
 Human BCMA cysteine rich domain.
 Xu L;
 14-JAN-2002; 2002US-0348962P.
07-FEB-2002; 2002US-0354966P.
13-AUG-2002; 2002US-0403364P.
 24-OCT-2002; 2002WO-US034376.
 (first entry)
 Shu H, Liu Y,
 WPI; 2003-403345/38
 Query Match
Best Local Similarity
Matches 34; Conserv
 WO2003035846-A2.
 Sequence 34 AA;
 Homo sapiens.
 24-OCT-2001;
 domain (CRD)
 20-NOV-2003
 01-MAY-2003
 ADA49366;
 Zhang G,
ADA49366
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Gaps

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34; Conservative

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The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method compises administering a specific binding partner for APRLL (GTO, a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (lasthma, hypersensitivity lung disease), drug and insect sting allergy, inflammatory bowel disease (Crohi's disease, collitis), solerodermia, autoimmune disease (multiple sclerosis, rheumatoid arthritis, solerodermia, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infillration of the skin or organs. The present sequence is mouse BCMA protein-human immunoglobulin For region fusion protein.
 Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family
 Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; procetate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; cronn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis; fusion protein; mouse.
 Mouse BCMA-human immunoglobulin Fc region fusion protein.
41
 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC
 Disclosure; Fig 10B; 94pp; English.
 AAE15489 standard; protein; 281
 12-MAY-2000; 2000US-0204039P.
27-JUN-2000; 2000US-0214591P.
14-MAY-2001; 2001US-00214591.
 14-MAY-2001; 2001WO-US015567
 (first entry)
 (revised)
 WPI; 2002-066686/09.
 (AMGE-) AMGEN INC.
 Yu G;
 WO200187979-A2.
 Homo sapiens
 29-AUG-2003
12-MAR-2002
 22-NOV-2001,
 rheill LE,
 AAE15489;
 Chimeric.
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 RESULT 33
AAE15489
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Homo sapiens
 22-APR-2004
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 19-JUN-2003
 invention
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 Best Loc
Matches
 AD153060
 RESULT
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 defined sequence in the specification. The composition is useful in modulating the activity of TALL-1, and in treating, preventing, ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or lymphoma. The composition may also be used in treating inflammations (e.g. rheumatoid arthitis), acute pancreatitis, Alzheimer's disease, asthma, atherosclerosis, cachexia, cirrhosis, diabetes, disease, glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis
 64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSG-------LLGMANIDLEKSR 108
 109 TGDEIILPRGLEYTVEECTCEDCIKSKPKVDSD------HCFPLPAMEE-----GAT 154
 81 PKDTLMISRTPEVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 137
 systemic lupus erythematosus; B-cell-mediated cancer; lymphoma; Inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis; Alzheimer's disease, asthma, cachexia; cirrhosis; diabetes; osteoporosis; glomerulonephritis; Hashimoto a chyroiditis; ischeemic injury; psoriasis;
 4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNA1LWTCLGLS 63
 47
 invention relates to a novel TALL-1-binding polypeptide comprising a
 multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
 New TALL-1-binding polypeptide, useful for modulating the activity of TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune diseases, cancers or lymphomas.
 1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGS-----
 Gaps
 protein; TALL-1; B-cell-mediated autoimmune disease;
 80;
 Length 281;
 54; Indels
 SVLTVLHODWLNGKEYKCKVSNKALPA-PIEKTIS 171
 19.4%; Score 187; DB 5; 29.8%; Pred. No. 2.9e-11; iive 17; Mismatches 54;
 ILVTTKTNDY-----CKSLPAALSATEIEKSIS
 TALL-1 related protein SEQ ID No 197.
 Disclosure; Page 26; 236pp; English.
 ₹
 ABJ38417 standard; protein; 42
 13-MAY-2002; 2002WO-US015273.
 11-MAY-2001; 2001US-0290196P
 entry)
 64; Conservative
 (first
 WPI; 2003-156719/15
 Similarity
 (AMGE-) AMGEN INC
Sequence 281 AA;
 WO200292620-A2.
 TALL-1-binding
 Heu H;
 Ното варіепв.
 therapy
 12-JUN-2003
 21-NOV-2002.
 ABJ38417;
 48
 138
 Query Match
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and vasculitis. Disorders may be treated with the novel composition using gene therapy. This sequence represents a TALL-1 related protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      crystalline Neutrokine-alpha protein, useful for designing compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer, allergic disorders, or autoimmune diseases such as rheumatoid arthritis, multiple sclerosis, Crohn's disease, diabetes, systemic lupus erythematosus or asthma. This sequence represents the residues in the receptor for binding a cytokine ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein co-ordinate data, cytostatic, antiallergic; immunosuppressive; antirheumatic; antiatthritic; neuroprotective; antinflammatory; antidiabetic; dermatological; antiasthmatic; neutrokine-alpha; crystallography; cancer; allergic disorder; autoimmune disease; rheumatoid arthritis; multiple sclerosis; Crohn's disease; diabetes; systemic lupus erythematosus; asthma; receptor.
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                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                Length 42;
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Best Local Similarity 100.0%; Pred. No. 9.1e-09;
Matches 26; Conservative 0; Mismatches n.
                                                                                                                                                                                                                           Pred. No. 3.1e-09;
                                                                                                                                                                                            Score 158; DB 6;
                                                                                                                                                                     16.4%; Sco...
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     MLQMAGQCSQNEYFDSLLHACIPCQLRC 42
                                                                                                                                                                                                                                                                                                                            1 MLQMAGQCSQNEYFDSLLHACIPCQLRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human BCMA receptor binding site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADI53060 standard; peptide; 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2002; 2002WO-US035661.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-.) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arnold E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                           Local Similarity 100.
1es 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-532895/50.
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allergic disorders.
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                                                                                                                                Sequence 42 AA;
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receptor (BAFF-R) protein.

(first entry)

25-JUL-2002 Murine BAFF

AAE22244;

AAE22244 standard; protein; 175 AA.

AAE22244

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TRAF3-binding B cell-specific receptor and encoded gene, applicable in diagnosis of abnormality due to TRAF3-mediated intracellular signal transduction and in screening drugs for e.g. cancer, autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse; TRAF3-binding B cell-specific receptor; TRAF3; signal transduction; TNF ligand; cancer; autoimmune disease; apoplexia; viral infection; AIDS; bone disease; transplantation rejection; Alzheimer's disease; ischaemia; rheumatoid arthritis; cachexia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a murine TRAF3-binding B cell-specific receptor. The polynucleotide and polypeptide sequence of this receptor are useful for diagnosis of abnormality due to TRAF3-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intracellular signal transduction and in screening drugs for diseases associated with TNF ligand family and TNF receptor-ligand superfamily e.g. cancer, autoimmune diseases, viral infections like AIDS, bone diseases, transplantation rejection, Alzheimer's disease, ischaemia, rheumatoid arthritis, apoplexia and cachexia
                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of murine TRAF3-binding B cell-specific receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 175;
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29.4%; Pred. No. 0.00056;
ive 21; Mismatches 64
EYFDSLLHACIPCOLRCSSNTPPLTC 37
                                                           26
                                EYFDSLLHACIPCQLRCSSNTPPLTC
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                                                                                                                                                                                                                      ABB78398 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2002; 2002WO-JP001849.
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                                                                                                                                                                                                                                                                                                                                               (first entry)
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N-PSDB; ABV72373.
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(IRIE/) IRIE S.
(SATO/) SATO T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sato T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 175 AA;
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                                                                                                                                                                                                                                                                                                                                               17-DEC-2002
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Best Local S:
Matches 50
                                                                                                                                                                                                                                                                                    ABB78398;
12
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Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; hyman immunodeficiency virus; genetic disorder; cardiovascular; TNF; renal; rheumatoid arthritis; systeme lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                             New human BAFF receptor proteins and nucleic acids, useful for treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal
                                                                             Murine; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation;
                                                                                                                                                                                                                 /label= Transmembrane domain
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                         18-SEP-2000; 2000US-0233152P.
21-SEP-2000; 2000US-0234140P.
13-FEB-2001; 2001US-026499P.
14-AUG-2001; 2001US-0312185P.
                                                                                                                                                                                                                                                                                   06-SEP-2001; 2001WO-US028006.
                                                                                                                                                                                                                                                                                                                                                                                      Thompson JS;
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-362428/39.
N-PSDB; AAD35411.
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                                                                                                                                                                      Mus musculus.
                                                                                                                                                                                                                                                                                                                              13-FEB-2001;
14-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                       Ambrose CM,
                                                                                                                                                                                                                                                              28-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders.
                                                                                                                                                                                                       Domain
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The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Fractor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune cancel sisease, anti-phospholipid syndrome, Wegener's granulomatosis, colls disorders e.g., multiple myelome, Wegener's granulomatosis, and canon-tracitis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myelome, Weldenstrom's, macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and concein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or of forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens tor pharmacogenomic) are further useful as immunogens to raise anti-BFFR activity or expression.

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Gaps

35;

64; Indels

Conservative

50;

Similarity

80

57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111 GLILALTLVGLVSLVSWRWRQQLRTASPDTSEGVQQE-----SLENVFVPSSET-- 129

112 BIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161

81

21 OCNOTECFOPLVRNCVSCELFHTPDTGHTSSLEPGTALOPQEGSALRPDVALLVGAPALL 7 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL

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Example 4; Fig 4b; 164pp; English.

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N-PSDB; ABZ68876
                                                                                                                                                                                                                               Sequence 175 AA;
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Local Sim.
50;
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                                                                                                                                                                                                                                                                                                                                                                                                                              130
                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a human tumour necrosis factor receptor designated Zinfril (1). (1) has cytostatic, immunosuppressive, dermatological, antiinflammatory, represprotective, antiidabetic, antirthritic, antiasthmatic, nephrotropic and bypotensive
                                                                                                                                           57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
                                                                                                                                                                   GLILALTLVGLVSLVSWRWRQQLRTASPDTSEGVQQE-----SLENVFVPSSET-- 129
                                                                                                                     21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated human tumor necrosis factor receptor polypeptide, termed 
Ztnfr 12, useful for treating autoimmune disorders, emphysema, end stage renal failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                           Human; Ztnfr12; tumour necrosis factor receptor; cytostatic; immunosuppressive; dermatological; antiniflammatory; antidiabetic; neuvoprotective; antirheumatic; antiarthritic; antidiabetic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour; autoimmune disorder; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthema; rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myelone; amphyloidosis; light chain neuropathy; hypotension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease.
                                                                                              7 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL
                                                                      Gaps
                                                                                                                                                                                             112 EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
                                                                                                                                                                                                          ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
                                                                      35;
                                             Length 175;
                                                                      64; Indels
                                             12.1%; Score 116.5; DB 5; 29.4%; Pred. No. 0.00056; ive 21; Mismatches 64;
The present sequence is murine BAFF-R protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grant FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 140; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                      Mouse Ztnfr12 protein SEQ ID NO:13.
                                                                                                                                                                                                                                                                                ABB81489 standard; protein; 175 AA
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20-DEC-2000; 2000US-0257131P.
28-UUN-2001; 2001US-0301715P.
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                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                      50; Conservative
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                                                           Similarity
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                         Sequence 175 AA;
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                                            Query Match
Best Local S
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activities, and can be used in gene therapy. (I) can be used for inhibiting, in a mammal, the activity of a ligand that binds Zuffr12 (e.g. ZTWF4), for treating disorders and diseases associated with B (ymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (I) is useful for treating autoimnume disorders such as systemic lupus erythematosus, mysathenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, rheumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal diseases such as sponenties, and for treating renal correspond any pyelonephyritis, vasculatis, chronic lymphoid leukaemia, nephritis, and pyelonephyritis, and for treating renal complasms, multiple myelones, lymphomas, light chain neuropathy, or modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and crown's disease. (I) is useful for modulating the immune system, for regulating B cell responses and development, for modulating development of other cells, antibody production and cytokine production, and for modulating T and B cell communication. The present sequence represents mouse Ztnfr12 which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 GLILALTLVGLVSLVSWRWRQQLRTASPDTSEGVQQB-----SLENVFVPSSET-- 129
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TALL-1; April; systemic lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 OCSQNEYFDSLLHACIPCOL-----GTNAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; Score 116.5; DB 5; llarity 29.4%; Pred. No. 0.00056; Conservative 21; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of murine BR3 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 9A; 153pp; English.
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WPI; 2002-362428/39

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                                                                                                                                                                                                                                                                                                    Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; senetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening;
                                                                                                                                                                                                                                                                                57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
           The present sequence represents a murine BR3 polypeptide. The specification also describes TACI polypeptides. TACI and BR3 are receptors. Tunnumers and BR3 are bind to the TACI receptor, while TNF family ligands TALL-1 and April bind to the TACI receptor, while TNF family ligands TALL-1 also binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for
                                                                                                                                                                                                                    7 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
                                                                                                                                                                                                                                                 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80
                                                                                                                                                                                      Gaps
                                                                                           preparing a composition for treating systemic lupus erythematosus
                                                                                                                                                                                                                                                                                                                                                                 ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
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                                                                                                                                                       Length 175;
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                                                                                                                                                      DB 6;
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                                                                                                                                                    12.1%; Score 116.5; DB 6
29.4%; Pred. No. 0.00056;
ive 21; Mismatches 64
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2001US-0268499P.
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                                                                                                                                                                                      Conservative
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                                                                                                                          Sequence 175 AA;
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13-FEB-2001;
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Best Local 6
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unmourspanic conditions or inherited genetic disorders involving breaths, the unmourspanic conditions or inherited genetic disorders, inflammation, organ transplantation and HIV. Autoimmune disorders, inflammation, organ transplantation and HIV. Autoimmune to diseases, which can be treated or prevented by BAFF.K. include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopaenia purpura, Chagas' disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammapathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in screening assays, in detection assays (chromosomal mapping, tissue typing or forenisc biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFFR antibodies, or in creening drugs or compounds that modulate BAFFR antibodies, or in the present sequence is human BAFFR protein mutant. Note: The present sequence is human BAFFR protein mutant. Note: The present sequence is human BAFFR protein mutant. Note: The present sequence is human BAFFR protein mutant is derived from human BAFFR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 SRIGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVIT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56 LW---TCLGLSLIISLAVFVLMF----LLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                                                          The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Mecrosis Pector (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic diseases involving B-cells, tumourigenic conditions or inherited genetic diseases.
                                          proteins and nucleic acids, useful for treating
                                                             preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSQNEYFDSLLHACIPCQL------RCSSNTPPLTC---QRYCNASVTNSVKGTNAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.0%; Score 106.5; DB 5; oc. 4%; Pred. No. 0.0071;
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                                                                                                                                                                Example 17; Page; 164pp; English.
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                                            human BAFF receptor
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Best Local Similarity
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renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening;
                                                                "Wild type Pro substituted with Gln"
                                                                            'note= "Wild type Ala substituted with Thr"
                                                    'note= "Wild type Val substituted with Asn"
                                         Location/Qualifiers
                                                                                                               06-SEP-2001; 2001WO-US028006.
                                                                  note=
                                                           Misc-difference
                                              Misc-difference
                                                                       Misc-difference
                  mutant; mutein
                                                                                        WO200224909-A2
                              sapiens
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18-SEP-2000; 2000US-0233152P. 21-SEP-2000; 2000US-0234140P. 13-FEB-2001; 2001US-0268499P. 14-AUG-2001; 2001US-0312185P.

(BIOJ) BIOGEN INC.

Thompson JS; WPI; 2002-362428/39. Ambrose CM,

New human BAFF receptor proteins and nucleic acids, useful for treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal disorders.

Example 17; Page; 164pp; English.

The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune Captoress, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, mysathenia gravis, autoimmune captoressive disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodose and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myeloma, Weldenstrom's macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and connoclonal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in streening assays, in detection assays (chromosomal mapping, tissue typing or forensic bloology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful a immunogens to raise anti-BFFR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant. Note: The present sequence is human BAFF-R protein mutant. Note: The present sequence is human BAFF-R protein mutant. Note: The present sequence is human BAFF-R protein mutant. Note: The present sequence is human BAFF-R protein mutant in fig 2d of the specification

Sequence 185 AA;

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8
                                 Gaps
                                 49;
   Length 185;
                                 Indels
/ Match 10.9%; Score 105.5; DB 5; Local Similarity 26.4%; Pred. No. 0.0091; nes 48; Conservative 23; Mismatches 62;
 Query Match
                                Matches
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CSQNEYFDSLLHACIPCQL-----RCSSNTPPLTC---QRYCNASVTNSVKGTNAI

55

107 SRTGDBIILPRGLEYTVEBCTC-----BDCIKSKPKVDSDHCPPLPAMBEGATILVTT 159 LW---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106 161 179 ğ ğ 26 79 129 160 178 셤 ઠે 셤 용 ò ద δ

AAE15487 standard; peptide; 21 AA RESULT 42 AAE15487

AAE15487;

(first entry) 12-MAR-2002 Human B-cell maturation (BCMA) protein transmembrane region.

Human; transmembrane activator and intracellular CAML interactor; TACI; cytostatic; B cell maturation protein; BCMA; tumour necrosis factor; TNF; lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic; prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis; drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease; Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer; rheumatoid arthritis; atherosclerosis.

Homo sapiens.

WO200187979-A2.

22-NOV-2001.

14-MAY-2001; 2001WO-US015567

12-MAY-2000; 2000US-0204039P. 27-JUN-2000; 2000US-0214591P. 14-MAY-2001; 2001US-00214591.

(AMGE-) AMGEN INC.

Yu G; Theill LE, WPI; 2002-066686/09.

Inhibiting activity of B cell maturation protein and/or transmembrane activator and intracellular cyclophilin ligand interactor, by administering a binding partner for APRIL, a tumor necrosis factor family ligand

Disclosure; Fig 10A; 94pp; English.

The invention relates to a method for inhibiting TACI (transmembrane activator and intracellular CAML interactor) and/or B cell maturation protein (BCMA) activity in a mammal. The method comprises administering specific binding partner for APRIL (GTO), a tumour necrosis factor-TNF family ligand), having the consensus region of TACI, BCMA, or the TACI/BCMA extracellular consensus sequence, but not the extracellular region of TACI or BCMA. The method is useful for inhibiting activity of TACI and/or BCMA in a mammal which is useful for treating B-cell or T-cell lymphoproliferative disorders, one or more solid tumours such as lung, gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI antagonists are useful for treating inflammation and immune function diseases such as diarrhoea, postiasis, allergies, pneumonia, atopic dermatitis, respiratory allergic disease (asthma, hypersensitivity lung

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF;
disease), drug and insect sting allergy, inflammatory bowel disease (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal, bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer with leucocyte infiltration of the skin or organs. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF is a B-cell activating factor belonging to the Tumour Necrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are
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                                                                                                                                                                                        Gaps
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                                                                                                                                                         Length 21;
                                                                                                                                                     Score 104; DB 5; Length 21
Pred. No. 0.00075;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human BAFF receptor (BAFF-R) mutant, V20N/P21Q.
                                                                                    is human BCMA protein transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                          AAE22269 standard; protein; 185 AA
                                                                                                                                         100.0%; Pre 0; 1
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                                                                                                                                                                                                                                           1 ILWTCLGLSLIISLAVFVLMF
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2001US-0268499P.
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                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                     Query Match 10.8
Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                     Sequence 21 AA;
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tumourigenic conditions or inherited genetic disorders involving B-cells, the present of disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune disorders, inflammation, organ transplantation and HIV. Autoimmune chaemolytic anaemia, idopathic prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, mysathenia gravis, autoimmune haemolytic anaemia, idopathic thrombocytopaemia purpura, chagas disease Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulonephritis. Plasma cells disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and chartering anopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in sortein, protein homologues, and antibodies may further be used in corening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or paramacogenemic). The polypeptides are further useful as immunogens to raise anti-BFRR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant. Note: The present sequence is human BAFF-R protein mutant. Note: The present sequence is human BAFF-R protein mutant. Note the present experience is not shown in the specification but is derived from human BAFF-R.
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useful for treating, preventing or delaying autoimmune diseases, cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.7%; Score 103.5; DB 5; 26.4%; Pred. No. 0.015; iive 23; Mismatches 62;
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nes 48; Conserv
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rheumatoid arthritis; systemic lupus erythematosus; B cell neoplasm; multiple myeloma; immune function; Antiarthritic; Immunosuppressive; Dermatological; Antiinflammatory; Pungicide; Protozoacide; Antibacterial; Virucide; Antidiarrheic; Antipsoriatic; Antiallergic; Antiasthmatic; Neuroprotective; Antidiabetic; Cytostatic.

Antirheumatic; tumor necrosis factor; apoptosis; TALL-1R;

ADB90663 standard; protein; 185 AA

ADB90663

ADB90663;

(first entry

04-DEC-2003 TALL-1R gene

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The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (TMF) family, which is associated with the expression of Decells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematoaus, rheumatoid arthritis, myasthenia gravis, autoimmune can be among the disorders of an include arthritis, myasthenia gravis, autoimmune can disease, anti-phospholiph dyndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulonephritis. Plasma calls disorders e.g., multiple myeloma, Waldenstrom & macolophulinamaia, monoclonal gammopathy of undetermined significance. The nucleic acids, protean, protein, protein, protein, and antibodies may further be used in carrenting assays in dartering assays (and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies may further be used in a contain and antibodies and antib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 screening assays, in detection assays (chromosomal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or parametery. The polypeptides are further useful as immunogens to raise anti-BFFR antibodies, or in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant. Note: The present sequence is not shown in the specification but is derived from human BAFF-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
                                                                                                                                                                                                                                                                                                                        New human BAFF receptor proteins and nucleic acids, useful for treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal
                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 17; Page; 164pp; English.
                                                                                                      21-SEP-2000; 2000US-0234140P.
13-FEB-2001; 2001US-0268499P.
14-AUG-2001; 2001US-0312185P.
                                         06-SEP-2001; 2001WO-US028006
                                                                                                                                                                                                                                      Thompson JS;
                                                                                                                                                                                                                                                                                    WPI; 2002-362428/39.
                                                                                                                                                                                           (BIOJ ) BIOGEN INC.
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                                                                                      18-SEP-2000;
                                                                                                                                                                                                                                        Ambrose CM,
28-MAR-2002
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20-SEP-2002; 2002WO-US030009. 21-SEP-2001; 2001US-0324238P.

WO2003024991-A2

Ношо

27-MAR-2003

WPI; 2003-421121/39.

N-PSDB; ADB90662

(AMGE-) AMGEN INC

Hen H;

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56 LW---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                                       LFGAPALIGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL----- 128
                                                                                                                                                                                                                            SRTGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTT 159
                                                                                                                                                                                                                                                                ----DKVII----LSPGISDATAPAWPPPGEDPGTTPP----GHSVPVPATELGSTELVTT 177
                                                                                                               CVQAECFDLLVRHCVACGLLRTPRPRPAGAASSPAPRTALQPQESVGAGAGEAALPLPGL 78
                                                                            8 CSQNEYPDSLLHACIPCQL------RCSSNTPPLTC---QRYCNASVTNSVKGTNAI
                                          49;
10.4%; Score 100.5; DB 5; Length 185; 26.4%; Pred. No. 0.031; ive 22; Mismatches 63; Indels 49
                                        48; Conservative
                      Similarity
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KT 179
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   Query Match
Best Local 8
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                                        Matches
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The present invention relates to a tumor necrosis factor and apoptosis ligand-related leukocyte-expressed ligand 1 receptor (ThLL-1R) bolypeptide of the invention is useful for treating, preventing, or ameliorating a medical disease, condition or disorder, preferably a TALL-1R polypeptide-related disease, where the disease condition or disorder is rheumatoid arthritis, systemic lupus condition or disorder is rheumatoid arthritis, systemic lupus inflammation or immune function. The polypeptide is useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject. The present sequence represents a TALL-1R gene of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SWRRRQQRLRGAASTE-- 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117 -APDGDKAAAAPEPLDKVIILSPGTTDATAPAWPPPGEDQGTTPPGHSIPVPATELGSTEL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NAILW---TCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLE 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 KSRTGDEIILPRGLEYTV--EECTCEDCIKSKPKVDSD-----HCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVPTECYDLLVRKCVDCRLLRKS--PPKTA----AGASSPAPGTALQPQESVGTGSGEV 71
Novel tumor necrosis factor and apoptosis ligand-related leukocyte-
expressed ligand 1 receptor polypeptide, useful for treating rheumatoid
arthritis, systemic lupus erythematosus, B cell neoplasm, or multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSONEYFDSLLHACI PCOLRCSSNTPPLTCORYCNASVTNSVKGT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 100; DB 7; Length 18
23.8%; Pred. No. 0.035;
ive 25; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 122; 130pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 23.84
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VITKT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention.
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                                                                                                                   myeloma.
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The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor (FMF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal disorders, inflammation, organ transplantation and HIV. Autoimmune of disorders, inflammation, organ transplantation and HIV. Autoimmune cancer, thematogus, rheumatoid arthritis, myasthenia gravis, autoimmune cancer, diseases, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulomatosis, calls disorders e.g., multiple myeloma, Maldenstrom's macroglobulinaemia, monoclomal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in the control of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myaethenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening;
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genetic disorders involving B-cells, cardiovascular disorders, or renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Wild type Val substituted with Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Wild type Ala substituted with Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human BAFF receptor (BAFF-R) mutant, V20N/A22T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                        AAE22268 standard; protein; 185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 17; Page; 164pp; English.
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2001US-0268499P.
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Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mutant; mutein.
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13-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                     AAE22268
RESULT 46
                                                    AAE22268
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          screening drugs or compounds that modulate BAFF-R activity or expression. The present sequence is human BAFF-R protein mutant. Note: The present sequence is not shown in the specification but is derived from human BAFF-R referred as SEQ ID NO: 5 (AAB22242) and shown in fig 2d of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Tumour Necrosis Factor; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular; renal; rheumatoid arthritis; systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening;
                                                                                                                                                                                                                                                                                                                           LW---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                                                                                                                                                            107 SRTGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTT 159
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are further useful as immunogens to raise anti-BFFR antibodies, or in
                                                                                                                                                                                         CSQNEYFDSLLHACIPCQL-----RCSSNTPPLTC---QRYCNASVTNSVKGTNAI
                                                                                                                                                                                                                    CNPTECFDLLVRHCVACGLLRTPRPKPAGAASSPAPRTALQPQESVGAGAGEAALPLPGL
                                                                                                                                                                                                                                                                               LFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL------
                                                                                                                                                               Gaps
                                                                                                                                                             49;
                                                                                                                                DB 5; Length 185;
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                                                                                                                                                            Indels
                                                                                                                                                            63;
                                                                                                                               10.3%; Score 99.5; DB 25.8%; Pred. No. 0.04;
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human BAFF receptor (BAFF-R) mutant, V20N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE22270 standard; protein; 185 AA.
                                                                                                                                                             23;
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2000US-0234140P.
2001US-0268499P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                               Conservative
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                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                   Sequence 185 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutant; mutein.
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                                                                         specification
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                                                                                                                                Query Match
Best Local
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/note= "Alternative splice acceptor site"

/note= "Four cysteine motif"

Misc-difference

Location/Qualifiers

Homo sapiens.

JST576.

Key Domain

/note= "Stop transfer signal"

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18-SEP-2000; 2000US-0233152P. 21-SEP-2000; 2000US-0234140P. 13-FEB-2001; 2001US-0268499P. 14-AUG-2001; 2001US-0312185P.

Thompson JS;

Ambrose CM,

(BIOJ) BIOGEN INC.

06-SEP-2001; 2001WO-US028006

WO200224909-A2

28-MAR-2002

73. .100 /label= Transmembrane_domain

/note= "Hydrophobic region"

100

Region Domain Region

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The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Decrosis Factor (TNF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins, DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumourigenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders, immunosuppressive diseases, renal diseases, which can be treated or prevented by BAFF-R, include systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis, autoimmune hamolytic anaemia, idiopathic thrombocytopaenia purpura, Chagas' disease Grave's disease, anti-phospholipid syndrome, Wegener's granulomatosis, poly-arteritis nodosa and rapidly progressive glomerulonatosis, calls disorders e.g., multiple myeloma, Waldenstrom's macroglobulinaemia, monoclomal gammopathy of undetermined significance. The nucleic acids, protein, protein homologues, and antibodies may further be used in processive delay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               screening assays, in detection assays (chromosomal mapping, tissue typing or foremaic biology), predictive medicine (e.g. diagnostic or prognostic assays, monitoring clinical trials, or pharmacogenomic). The polypeptides are further useful as immunogens to raise anti-BFR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is human BAPP-R protein mutant, Note: The present sequence is not shown in the specification but is derived from human BAPP-R referred as SEQ ID NO: 5 (AAE22242) and shown in fig 2d of the
preventing or delaying e.g. autoimmune diseases, cancers, inherited
genetic disorders involving B-cells, cardiovascular disorders, or renal
                                                                                                               Example 17; Page; 164pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 185 AA;
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LW---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                         SRTGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTT 159
                                                                    CSQNEYFDSLLHACIPCQL-----RCSSNTPPLTC---QRYCNASVTNSVKGTNAI 55
                                                                                                                                 LFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL-----
                            49;
10.1%; Score 97.5; DB 5; Length 185; 25.8%; Pred. No. 0.065; tive 23; Mismatches 63; Indele 49
                         23;
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             Similarity
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Human; BAFF receptor; BAFF-R; cytostatic; hypotensive; inflammation; TNF; Humour Necrosis Pector; autoimmune disease; immunosuppressive; cancer; myasthenia gravis; hypertension; organ transplantation; drug screening; HIV; human immunodeficiency virus; genetic disorder; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                              renal; rhoumatoid arthritis, systemic lupus erythematosus; amyloidosis; haemolytic anaemia; Chagas' disease; Grave's disease; glomerulonephritis; multiple myeloma; chromosomal mapping; tissue typing; drug screening;
                                                                                                                                                                                                             Human mature JST576 (BAFF-R) protein.
                                                 AAE22242 standard; protein; 185 AA.
                                                                                                                                                         (first entry)
                                                                                                                                                         25-JUL-2002
                                                                                                     AAE22242;
RESULT 48
                   AAB22242
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CSQNEYFDSLLHACIPCOL-----RCSSNTPPLTC---QRYCNASVTNSVKGTNAI 55

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The invention relates to human BAFF receptor (BAFF-R) nucleic acids and proteins. BAFF-R is a B-cell activating factor belonging to the Tumour Necrosis Factor TANF) family, which is associated with the expression of B-cells and immunoglobulins. The BAFF-R proteins. DNA and antibodies are useful for treating, preventing or delaying autoimmune diseases, cancer, tumouriqenic conditions or inherited genetic disorders involving B-cells, hypertension, cardiovascular disorders immunosuppressive diseases, renal diseases, which can be treated or prevented by BAFF-R, include systemic clupus erythematosus. Thematoid arthritis, mysathenia gravis, autoimmune haemolytic anaemia, idiopathic thrombocytopaenia purpura, Chagas' disease Grave's disease, anti-phospholipid syndrome, Negener's granulomatosis, colls disorders e.g., multiple myeloma, Waldenstrom's, macroglobulinaemia, heavy-chain disease, primary or immunocyte-associated amyloidosis, and monoclonal gammopathy of undetermined significance. The nucleic acids, cortion protein homologues, and antibodies and ristals, and monoclonal mapping, tissue typing or forensic biology), predictive medicine (e.g. diagnostic or prognostic are further useful as immunogene traits anti-BFFR antibodies, or in screening drugs or compounds that modulate BAFF-R activity or expression.

The present sequence is human mature JST576 (BAFF-R) protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human BAFF receptor proteins and nucleic acids, useful for treating, preventing or delaying e.g. autoimmune diseases, cancers, inherited genetic disorders involving B-cells, cardiovascular disorders, or renal
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25.8%; Pred. No. 0.14;
ive 22; Mismatches 64; Indels 49
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les 47; Conservative
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autoimmune disorders such as systemic lupus erythematosus, myasthenia gravis, multiple sclerosis, insulin dependent diabetes mellitus, asthma, theumatoid arthritis, bronchitis, emphysema and end stage renal failure or renal disease such as glomerulonephritis, vasculitis, chronic lymphoid leukaemia, nephritis, and pyelonephritis, and for treating renal neoplasms, multiple myelomas, lymphomas, light chain neuropathy, or amyloidosis, hypertension, large vessel disease, graft-versus host disease, graft rejection and crhon's disease, (I) is useful for modulating the immune system, for regulating B cell responses and production and crhon's disease (I) is useful for production and cytokine production, and for modulating E cell response and production and cytokine production, and for modulating T and B cell communication. Human Ztnfr12 is located to chromosome 22q13.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTGDEIILPRGLEYTVEECTC-----BDCIKSKPKVDSDHCFPLPAMEEGATILVTTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane activator; calcium modulator; nephrotropic; antibacterial; TACI; tumour necrosis factor-like protein; ZTNF2; ZTNF4; immunoglobulin; anaemia; gene therapy; cytostatic; antiinflammatory; immunosuppressive; glomerulonephritis; asthma; bronchitis; graft rejection; septic shock; dermatological; neuroprotective; cyclophilin ligand-interactor; human; autoimmune disease, systemic lupus erythematosus; multiple sclerosis; diabetes mellitus; rheumatoid arthritis; renal disease; inflammation;
                                                                                                                                                                                                                                                                                                                                                                 8 CSQNEYFDSLLHACIPCQL-----RCSSNTP--PLTCQRYCNASVTNSVKGTNAIL
                                                                                                                                                                                                                                                                                                                                                                                                        CVPAECFÖLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGEAALPLPGLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL------
                                                                                                                                                                                                                                                                                          Length 184;
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26.5%; Pred. No. 0.2;
tive 20; Mismatches
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nes 48; Conserva
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                                                                                                                                                                                                                                                        Sequence 184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a human tumour necrosis factor receptor designated Ztnfr12 (1). (1) has cytostatic, immunosuppressive, designated Ztnfr12 (1). (1) has cytostatic, immunosuppressive, antidiabetic, antidiabetic, neutrorective, antidiabetic, antidiabetic, antidiabetic, antidiathmatic, nephrotropic and hypotensive activities, and can be used in gene therapy. (1) can be used for inhibiting, in a mammal, the activity of a ligand that binds Ztnfr12 (e.g. ZTNF4), for treating disorders and diseases associated with B lymphocytes, activated B lymphocytes or resting B lymphocytes, and for inhibiting the proliferation of tumour cells. (1) is useful for treating
                                                                                                                                            CVPAECFDLLVRHCVACGLLRTPRPKPAGAASSPAPRTALQPQESVGAGAGEAALPLPGL 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isolated human tumor necrosis factor receptor polypeptide, termed 12, useful for treating autoimmune disorders, emphysema, end stage failure or renal disease and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disorder; systemic lupus erythematosus; myasthemia gravis; multiple sclerosis; insulin dependent diabetes mellitus; asthma; rheumatoid arthitis; bronchitis; emphysema; renal disease; lymphoma; glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis; pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis; light chain neuropathy; hypertension; large vessel disease; graft-versus host disease; graft rejection; Crohn's disease;
                                           LW---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEK
                                                                                                                      SRTGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTT
                                                                                LFGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPEPL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive; dermatological; antiinflammatory; antidiabetic; neuroprotective; antirheumatic; antiarthritic; antiasthmatic; nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Ztnfr12; tumour necrosis factor receptor; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Grant FJ;
                                                                                                                                                                                                                                                                                                                               ABB81483 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Ztnfr12 protein SEQ ID NO:2.
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20-DEC-2000; 2000US-0257131P.
28-JUN-2001; 2001US-0301715P.
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activator and calcium modulator and cyclophilin ligand-interactor (TACI) receptor group that binds tumour necrosis factor-like protein (ZTMP) or ZTMF4; and an immunoglobulin group comprising a constant region of an immunoglobulin. The invention is used to manufacture a medicament for inhibiting the proliferation of tumour cells in a mammalian subject. The composition comprising the fusion protein may also be used in treating autoimmune diseases (e.g. systemic lupus erythematosus, multiple autoimmune diseases (e.g. systemic lupus erythematosus, multiple sclerosis, diabetes mellitus, rheumatoid arthritis and asthma), renal diseases (e.g. glomerulonephritis), bronchitis, inflammantion, graft rejection, anaemia and septic shock. The fusion proteins are also used in gene therapy. The present sequence is human Ztnfr12 receptor protein
interactor (TACI)-immunoglobulin fusion protein, for treating cancer or diabetes, comprises a TACI receptor group and an immunoglobulin group.
                                                                                                                                                         The invention relates to fusion proteins comprising transmembrane
                                                                                            Disclosure; Col 136-137; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 184 AA;
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Query Match 9.6%; Score 93; DB 6; Length 184; Best Local Similarity 26.5%; Pred. No. 0.2; Matches 48; Conservative 20; Mismatches 65; Indels ሯ

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57 W---TCLGLSLIISLAVFVLMF-----LLRKISSEPLKDEFKNTGSGLLGMANIDLEKS 107

108 RIGDELLLPRGLEYTVBECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTTK 160

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Compugen Ltd.
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US-09-855-158-21
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Copyright (c) 1993 - 2005
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Sequence 6, Application US/09855158;
Sequence 6, Application US/09855158;
Sequence 6, Application No. US20020066018A1
GENERAL INFORMATION:
THELL INFORMATION:
TILLS OF INVENTION:
THENGER APPLICATION NUMBER: US 60/204,039
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLXS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT PAPLICATION NUMBER: US/99/854,864
CURRENT FILING DATE: 2000-09-11
PRIOR PELICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
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                                                                           Length 34;
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                                                                                                                       Indels
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                                                                    ; Score 201; DB 9;
; Pred. No. 2.2e-17;
0; Mismatches 0;
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100.0%; Score 201; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.3e-17;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                   1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                            US-09-854-864-6
; Sequence 6, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INFORMATION:
                                                                      Query Match
Best Local Similarity 100.0%;
Matches 34; Conservative 0
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ORGANISM: Homo sapiens
    ORGANISM: Homo sapiens
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            US-09-855-158-7
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| Bequence 7, Application US/09855158
| Publication No. US2000086018A1
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EVDE
| APPLICANT: THEILL, LARS EVDE
| APPLICANT: THEILL, LARS EVDE
| TITLE OF INVENTION: 3, AND TACI
| TITLE OF INVENTION: 3, AND TACI
| TITLE OF INVENTION: 3, AND TACI
| TITLE OF ILING DATE: 2000-09-11
| FILE REFERENCE: A-666A
| CURRENT FILING DATE: 2000-06-27
| PRIOR FILING DATE: 2000-06-12
| PRIOR PLING DATE: 2000-05-12
| PRIOR PLING DATE: 2000-05-12
| NUMBER OF SEQ ID NOS: 30
| SCOFTWARE: Patentin version 3.1
| LENGTH: 34
| TYPE: PRI
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US-09-854-864-7

US-09-854-864-7

Saduence 7, Application US/09854864

Patent No. US20020081296A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EXDE

APPLICANT: THEILL, LARS EXDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLXS/AGP-3, AND TACI

FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR PLING DATE: 2000-05-12

PRIOR PLING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PRECETIN VERSION 3.1

SOFTWARE: PRECETIN VERSION 3.1

SOFTWARE: PRECETIN VERSION 3.1
                     Sequence 12, Appl
Sequence 12, Appl
Sequence 234, Appl
Sequence 35, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 2874, Appl
Sequence 36, Appl
Sequence 36, Appl
Sequence 36, Appl
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                   US-09-898-570-12

US-09-839-446-12

US-10-1040-407-2834

US-10-239-663-35

US-10-470-390A-12

US-10-470-390A-12

US-10-480-172-22

US-09-898-570-14

US-09-839-446-14

US-09-839-446-14

US-09-839-446-14

US-09-839-446-14

US-10-239-663-36

US-10-239-663-36

US-10-406-073-8

US-10-406-073-15
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ilarity 100.0%; Pred. No. 2.2e-17;
Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-09-854-864-7
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Best Local Similarity
Matches 34; Conserv
  US-09-855-158-7
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Sequence 13, Application US/09855158

Sequence 13, Application US/09855158

Publication No. US20020086018A1

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EXDE

APPLICANT: TV, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL'

TITLE OF INVENTION: 3, AND TACI

TITLE OF INVENTION NUMBER: US/09/855,158

CURRENT FILING DATE: 2001-06-27

PRIOR PELICATION NUMBER: US 60/204,039

PRIOR FILING DATE: 2000-06-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Version 3.1

SEQ ID NO 13
                                      APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: TYU, GAN
TITLE OF INVENTION: BLYS/AGP-1, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR PLILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 13
LENGTH: 81
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APPLICANT: YU, GANG
TITLE OF INVENTION: BLXS/AGP-3, AND TACI
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Pred. No. 5.1e-17;
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100.0%; Score 201; D
Best Local Similarity 100.0%; Pred. No. 5.1
Matches 34; Conservative 0; Mismatches
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Application US/09854864
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Patent No. US20020081296A1
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Best Local Similarity
Matches 34; Conserv
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US-09-855-158-13
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US-09-854-864-13
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; Sequence 21, Application US/0985158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
APPLICANT: YU GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
; TITLE OF INVENTION: 3, AND TACI
; FILE REPRENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: PALOR NUMBER: US 60/204,039
; SOFTWARE: PALOR LING DATE: 2000-05-12
; REGION OF SEQ ID NOS: 30
; SOFTWARE: PALOR LIN Version 3.1
; SEQ ID NO 21
                                                                                                                                                                                                                                     APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS AND
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLXS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PILLING DATE: 2000-05-12
PRIOR PILLING DATE: 2000-05-12
PRIOR PILLING DATE: 2000-05-17
PRIOR PILLING DATE: 2000-06-17
PRIOR FILLING DATE: 2000-06-17
SOFTWARE: PARENT OF SEQ ID NOS: 31
SOFTWARE: PARENT OF SEQ ID NOS: 31
LENGTH: 58
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100.0%; Score 201; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.7e-17;
Matches 34; Conservative 0; Mismatches 0;
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                                                                                                                                                                Sequence 21, Application US/09854864 Patent No. US20020081296A1 GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-855-158-21
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ORGANISM: Homo sapiens
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Best Local Similarity
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100.0%; Pred. No. 1.1e-16;
rative 0; Mismatches 0;
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100.0%; Pred. No. 1.1e-16;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Thompson, uctily
APPLICANT: Thompson, uctily
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080FCT
CURRENT PPLICATION NUMBER: U5/10/077,438
CURRENT PPLING DATE: 2002-02-18
PRIOR APPLICATION NUMBER: 60/19,378
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR PLING DATE: 2000-02-11
PRIOR PLING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
                                  PRIOR APPLICATION NUMBER: 60/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR PELING DATE: 1999-08-17
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO II
CURRENT APPLICATION NUMBER: US/10/077,438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/10077438 Publication No. US20020165156A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/10077137; Publication No. US20020172674A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Browning, Jeffrey
Ambrose, Christine
Tschopp, Jurg
Schneider, Pascal
Thompson, Jeffrey
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Best Local Similarity 100.0
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                 ; ORGANISM: homo sapien
US-10-077-438-1
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ORGANISM: homo sapien
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APPLICANT:
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
TITLE OF INVENTION: METHODS AND TACI
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR PAPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PALENTH VERSION 3.1
SEQ ID NO 5.
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100.0%; Score 201; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
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APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
APPLICANT: Apotech R&D S.A.
APPLICANT: APOTECH R&D S.A.
APPLICANT: APOTECH R&D S.A.
A
                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
             CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5, Application US/09855158 Publication No. US20020086018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10077438 Publication No. US20020165156A1
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APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-5
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US-09-855-158-5
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Ambrose, Christine

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APPLICATE RUDEN, Steven M.

TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REFERENCE: PFS54
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT APPLICATION NUMBER: 60/293,100
PRIOR APPLICATION NUMBER: 60/293,100
PRIOR APPLICATION NUMBER: 2001-05-24
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
SEQ ID NO 4.7
ILBNGTH: 184
TYPE: PRI
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                                                Sequence 2, Application US/10068725
Fublication No. US20030012783A1
Fublication No. US20030012783A1
Fublication No. US20030012783A1
Fublication No. US20030012783A1
TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI
FILE REFERENCE: 01-04
CURRENT APPLICATION NUMBER: US/10/068,725
CURRENT FILING DATE: 2002-02-06
FRIOR PELING DATE: 2001-02-20
FRIOR PELING DATE: 2001-02-20
FRIOR PELING DATE: 2001-04-12
NUMBER OF SEQ ID NOS: 5
COFTWARE: FastSEQ for Windows Version 3.0
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Publication No. US20030082175A1
GENERAL INFORMATION:
APPLICANT: Apocter R & D S.A.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof FILE REFERENCE: A0819TCT
CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02
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Publication No. US20030059862A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
LENGTH: 184
TYPE: PRT
ORGANISM: Homo sapiens
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US-10-151-882-47
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Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 1.1e-16;
Michael Chebe
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                                      APPLICANT: intempoun, cerric,
APPLICANT: Biogen, Inc.
APPLICANT: Bootech Rad S.A.
TITLE OF INVENTION: Baff Receptor (BCWA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION OF THE COLO-15
FRIOR APPLICATION NUMBER: 60/149,378
FRIOR FILING DATE: 1999-08-17
FRIOR PILING DATE: 2000-02-11
FRIOR PILING DATE: 2000-02-11
FRIOR PILING DATE: 2000-02-11
FRIOR PILING DATE: 2000-02-11
FRIOR FILING DATE: 2000-02-11
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APPLICANT: MacKay, Fabienne
APPLICANT: Browning, Jeffrey
APPLICANT: Abhorse, Christine
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A080PCT
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PRIOR APPLICATION NUMBER: 60/149,378

PRIOR FILING DATE: 1999-08-17

PRIOR FILING DATE: 2000-02-11

PRIOR FILING DATE: 2000-02-11

PRIOR PLING DATE: 2000-02-11

PRIOR PLING DATE: 2000-02-11

SPRIOR PLING DATE: 2000-02-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 7
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Schneider, Pascal
Thompson, Jeffrey
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Best Local Similarity 100.
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: homo sapien
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ORGANISM: homo sapien
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| Publication No. US20030092164A1
| GENERAL INFORMATION
| APPLICANT: Gross, Jane A. APPLICANT: Ku, Wenfeng
| APPLICANT: Henne, Randal M. APPLICANT: Henne, Randal M. APPLICANT: Henne, Randal M. TITLE OF INVERTION: Human Tumor Necrosis Factor Receptor FILE REFERENCE: 00-103
| CURRENT PELING DATE: 2001-11-05
| NUMBER OF SEQ ID NOS: 46
| SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-152-363A-27

Sequence 27, Application US/10152363A

Publication No. US20030103986A1

GENERAL INFORMATION:

APPLICANT: Rixon, Mark W.

ITLE REPERENCE: 01-20

FILE REPERENCE: 01-20

CURRENT APPLICATION NUMBER: US/10/152,363A

CURRENT FILING DATE: 2002-05-20

PRIOR FILING DATE: 2001-05-24

NUMBER OF SEQ ID NOS: 70

SOFTWARE: RateSEQ for Windows Version 3.0

LENGTH: 184
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                                                                                                                                                                                                                                                                                                            0; Mismatches
                 PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/181807
PRIOR FILING DATE: 2000-02-11
PRIOR PILING DATE: 1090-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICATION NUMBER: 60/215688
                                                                                                                                                                                                                                                                                                          34; Conservative
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CORGANISM: Homo sapiens
US-10-008-063-7
                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-115-192-8
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ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                        Best Local Similarity
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US-10-008-063-7
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APPLICANT: Markwitz, Sanford David
APPLICANT: Markwitz, Sanford David
APPLICANT: Markwitz, Sanford David
APPLICANT: Markwitz, Sanford David
APPLICANT: Ease Western Reserve University
TITLE OF INVENTION: Caneer, Compositions and Methods of Screening for
TITLE OF INVENTION: Caneer, Compositions and Methods of Screening for
TITLE OF INVENTION: Caneer, Compositions and Methods of Screening for
TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer,
TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer
CURRENT FILING DATE: 2001-02-25
PRIOR APPLICATION NUMBER: US 60/281,149
PRIOR PILING DATE: 2001-04-02
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 41
SOFTWARE PATENTION OF SEQ ID NOS: 41
SEQ ID NO 39
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/10/216,074
CURRENT PRILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US/99/565,423
PRIOR PELING DATE: 2000-06-05
PRIOR PELING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 2000-06-07
PRIOR FILING DATE: 1999-05-06
SPRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN UNCY. 2.1
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                                                                    Gaps
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FEATURE:
OTHER INFORMATION: tumor necrosis factor receptor superfamily, member
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Length 184;
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   Score 201; DB 14;
Pred. No. 1.1e-16;
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100.0%; Score 201; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                        CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 41
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                                                                0; Mismatches
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Publication No. US20030148445A1
GENERAL INFORMATION:
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. Sequence 39, Application US/10087080
. Publication No. US20030235820A1
. GENERAL INFORMATION:
Query Match
Best Local Similarity 100.0%;
Matches 34; Conservative 0
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TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL.
TITLE OF INVENTION: 3, AND TACI
FILE REPERENCE: A-666A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN NUMBER: US 60/204,039
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APPLICANT: Apotech R & D S.A.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
FILE REFERENCE: A083PCT
CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT PILING DATE: 2002-04-02
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: 60/181807
PRIOR APPLICATION NUMBER: 60/18193
PRIOR APPLICATION NUMBER: 60/18193
SROID NOS: 12
SEQ ID NOS: 12
SEQ ID NOS: 12
SEQ ID NOS: 12
     Indels
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100.0%; Score 201; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.8e-16;
Mâtches 34; Conservative 0; Mismatches 0;
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                                                        1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
                                                                                                      5 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 38
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     0; Mismatches
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Publication No. US20030082175A1
GENERAL INFORMATION:
                                                                                                                                                                                                                               Sequence 9, Application US/09855158 Publication No. US20020086018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                             APPLICANT: THEILL, LARS EYDE APPLICANT: YU, GANG
     34; Conservative
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US-09-855-158-9
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ORGANISM: homo sapiens
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     Matches
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APPLICANT: Yeh, Ren-Hwa
APPLICANT: Yeh, Ren-Hwa
APPLICANT: Salperina, Olga
APPLICANT: Hibbert, David
APPLICANT: Hibbert, David
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Neutrockine-alpha Conjugate, Neutrokine-alpha Complex, and Uses Th
TITLE REFERENCE: 1488.1810.02
CURRENT APPLICATION NUMBER: US/10/742,634
CURRENT APPLICATION NUMBER: US 60/435,262
PRIOR APPLICATION NUMBER: US 60/435,262
PRIOR APPLICATION NUMBER: US 60/467,198
PRIOR FILING DATE: 2003-12-23
PRIOR FILING DATE: 2003-15-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THELL, LARS BYDE
APPLICANT: THELL, LARS BYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT FILING NAMER: US 60/204,039
FRIOR APPLICATION NUMBER: US 60/204,039
FRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
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Pred. No. 1.7e-16;
                                                                                                                                 Indels
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                                                                           Query Match 100.0%; Score 201; DB 14; Best Local Similarity 100.0%; Pred. No. 1.1e-16; Matches 34; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 1.1e-16;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/10742634 Publication No. US20040208824A1
; OTHER INFORMATION: 17 (TNFRSF17)
US-10-087-080-39
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SOFTWARE: Patentin version 3.1
SEQ ID NO 9
LENGTH: 283
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Matches 34; Conservative
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US-09-854-864-9
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ORGANISM: Homo sapiens
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Best Local Similarity
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Sequence 11, Application US/09855158
Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YO, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BLA
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
                                                                                                                                                                                                                                                                                                                                APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6668
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PLILNG DATE: 2000-05-12
PRIOR PLILNG DATE: 2000-05-12
PRIOR PLILNG DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-13
SEQ ID NOS: 31
SOFTWARE: PATENTIN NUMBER: US 60/214,591
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 11
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Length 207;
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Pred. No. 9.3e-09;
2; Mismatches 6; Indels
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Pred. No. 9.3e-09;
2; Mismatches 6; Indels
                                                 Indels
  Score 181; DB 13;
Pred. No. 3.4e-14;
0; Mismatches 0;
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 11
                                                                                                                                                                                                                                                           Sequence 11, Application US/09854864 Patent No. US20020081296A1 GENERAL INFORMATION:
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70.6%;
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70.6%;
    Query Match
Best Local Similarity 63.0%;
Matches 34; Conservative
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Best Local Similarity 70.6%
Matches 24; Conservative
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Best Local Similarity 70.63
Matches 24; Conservative
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CRGANISM: Murine
US-09-854-864-11
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US-09-855-158-11
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APPLICANT: Machose, Christine
APPLICANT: Tachopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Browning, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Bogen, Inc.
APPLICANT: Bogen, Inc.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
TITLE OF INVENTION: Daffs: 2001-02-15
CURRENT APPLICATION WUMBER: 60/149, 378
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR PILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PASCAGE OF Windows Version 4.0
SEQ ID NO 3
LENGTH: 207
                                                                                                                                       APPLICANT: MacKay, radicante APPLICANT: MacKay, radical APPLICANT: Ambrose, Christine APPLICANT: Tachopp, Jurg APPLICANT: Schneider, Pascal APPLICANT: Schneider, Pascal APPLICANT: Thompson, Jeffrey APPLICANT: Biogen, Inc. APPLICANT: Biogen, Inc. TITLE OF INVENTION: Baff Receptor (BCMA), An TITLE OF INVENTION: Immunoregulatory Agent TITLE OF INVENTION: Immunoregulatory Agent CURRENT APPLICATION NUMBER: 60/149,378 PRIOR PELICATION NUMBER: 60/149,378 PRIOR FILING DATE: 2000-02-11 PRIOR FILING DATE: 2000-02-11 PRIOR FILING DATE: 2000-02-11 PRIOR FILING DATE: 2000-02-18 NUMBER OF SEQ ID NOS: 8

SOFTWARE PASCAL OF WINDOWS OF SEQ ID NOS: 8

LENGTH: 207
                                                 Sequence 3, Application US/10077438 Publication No. US20020165156A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10077137
Publication No. US20020172674A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MacKay, Fabienne
APPLICANT: Browning Teff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: homo sapien
US-10-077-438-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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APPLICANT: THELLY, LARS EYDE
APPLICANT: THELLY, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL.
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-686A
CURRENT APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-6868
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MIN, HOSUNG
APPLICANT: HIN, HOSUNG
APPLICANT: HSU, HALLING
APPLICANT: ZIONG, FEI
TITLE OF INVENTION: PEPTIDES AND RELATED MOLECULES THAT BIND TO TALL-1
FILE REFERENCE: A-743
FURREW APPLICATION NUMBER: US/10/145,206
CURREWY APPLICATION NUMBER: US 60/290,196
PRIOR FILING DATE: 2001-05-13
NUMBER OF SEQ ID NOS: 197
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 281;
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Pred. No. 6.5e-08;
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Pred. No. 1.4e-08;
2; Mismatches 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 197, Application US/10145206
Publication No. US20030195156Al
GENERAL INFORMATION:
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Patent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS BYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 CSÓNEYFDSLLHACIPCOLRC 42
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  US20020086018A1
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Best Local Similarity 70.6%;
Matches 24; Conservative
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US-09-855-158-10
  Publication No. US200
GENERAL INFORMATION:
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS-10-145-206-197
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Fatent No. US20020081296A1

GENERAL INPORMATION:
GENERAL INPORMATION:
THELL, LARS EXDE

APPLICANT: THEILL, LARS EXDE

TITLE OF INVENTION:
FILE REFERENCE: A-686B

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

FILE REPLIAND DATE: 2000-05-12

PRIOR PLING DATE: 2000-05-12

PRIOR PLING DATE: 2000-05-13

PRIOR PLING DATE: 2000-06-77

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin version 3.1

SEQ ID NO 10

LENGTH: 281
                                                                                                                  Sequence 17, Application US/10216074

Publication No. US20030148445A1

Publication No. US20030148445A1

GENERAL INFORMATION:

APPLICANT: Shu, Hong-Bing

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: METHODS OF USE THEREOF

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT PILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-05

PRIOR FILING DATE: 2000-05-01

PRIOR FILING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PATCHIN VENTION OF 17

SOFTWARE: PATCHIN VENTION OF 2013

SOFTWARE: PATCHIN OF 2013
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Pred. No. 1.4e-08;
2; Mismatches 6; Indels
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  CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36
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US-09-855-158-10
; Sequence 10, Application US/09855158
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Best Local Similarity 70.6%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-10-216-074-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 24; Conserv
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| GENERAL INFORMATION: GENERAL INFORMATION: Reith D. |
| APPLICANT: Allen, Keith D. |
| TITLE OF INVENTION: SPGS SERINE PROTEASE GENE DISRUPTIONS, TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO |
| TITLE OF INVENTION: AND COMPOSITIONS AND METHODS RELATED THERETO |
| FILE REFERENCE: R-720 |
| CURRENT APPLICATION NUMBER: US 60/300,978 |
| PRIOR APPLICATION NUMBER: US 60/300,978 |
| PRIOR PELLING DATE: 2001-06-26 |
| PRIOR APPLICATION NUMBER: US 60/304,820 |
| PRIOR APPLICATION NUMBER: US 60/324,820 |
| NUMBER OF SEQ ID NOS: 4 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 2 |
| SEG ID NO 2 |
| SEQ ID NO 3 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
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                                                                                                                                                              Length 249;
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                                                                                                                                                                                                                                 Indels
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                                                                                                                                                              Score 71.5; DB 13;
Pred. No. 0.89;
8; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 33.6%; Score 67.5; DB 14; Best Local Similarity 37.8%; Pred. No. 16; Matches 14; Conservative 4; Mismatches 14;
                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                      1 CSONEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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APPLICANT: BOYLE, WILLIAM; APPLICANT: BOYLE, MILLIAM
APPLICANT: A-570B; FILE REPERBNCE: A-570B; CURRENT APPLICATION NUMBER: US/09/779,050A; CURRENT FILING DATE: 2001-02-12; PRIOR FAPLICATION NUMBER: 60/181,800; PRIOR FILING DATE: 2000-02-11; NUMBER OF SEQ 1D NOS: 52; SOFTWARE PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/10180903
Publication No. US20030093824A1
                                                                                                                                                                    35.6%;
                                                                                                                                                                    Query Match
Best Local Similarity 35.3
Matches 12; Conservative
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US-09-779-050A-45
                                        ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Mus Musculus
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          LENGTH: 249
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; Sequence 12, Application US/0985158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
A APPLICANT: YU. GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI
TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT PILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-06-27
; PRIOR FILING DATE: 2000-06-12
; PRIOR FILING DATE: 2000-06-12
; RUNDER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 0.0009;
1; Mismatches 2; Indels
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| Publication No. US20020182586A1
| GENERAL INPORMATION:
| APPLICANT: MOTIS, David W. |
| APPLICANT: Engelhard, Eric K. |
| TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR |
| TITLE OF INVENTION: CANCER |
| FILE REFERENCE: 529452000122 |
| CURRENT FILING DATE: 2002-03-01 |
| PRIOR APPLICATION NUMBER: US 09/747,377 |
| PRIOR FILING DATE: 2000-103-02 |
| NUMBER OF SEQ ID NOS: 2059 |
| SOFTWARE: FastSEQ for Windows Version 4.0 |
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Pred. No. 0.0009;
1; Mismatches 2;
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PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 117
                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: human-murine Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : human-murine Consensus
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1 Similarity 69.7%;
23; Conservative
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Matches 23; Conservative
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ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 8
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2 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 34

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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: 3, AND TACI
TITLE OF INVENTION: 3, AND TACI
TITLE OF INVENTION: 3, AND TACI
FILE REPRENCE: A-686A
CURRENT PILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-27
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-05-12
APPLICANT: THEILL, LARS EVDE
APPLICANT: THEILL, LARS EVDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: MEXS/AGP-3, AND TACI
FILE REFERENCE: A-6668
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PLING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 16
LENGTH: 67
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Batent No. US20020081296A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EVDE
APPLICANT: THEILL, LARS EVDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLXS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
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32.4%; Pred. No. 1;
:ive 8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 66.5;
Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16, Application US/09855158 Publication No. US20020086018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.1%;
Best Local Similarity 32.4%;
Matches 11; Conservative
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Best Local Similarity 32...
Best 11; Conservative
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; ORGANISM: Homo sapiens
US-09-855-158-16
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US-09-854-864-16
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; Publication No. US20020086018A1
; GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: THEILL, LARS EYDE
; APPLICANT: THEILL, LARS EYDE
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING AFRIL/G70, BCMA, BI
TITLE OP INVENTION: 3, AND TACI
; TITLE OP INVENTION: 3, AND TACI
; TITLE OP INVENTION: 3, AND TACI
; TITLE OP INVENTION: 3, AND TACI
; TITLE OP INVENTION: 3, AND TACI
; TITLE OP INVENTION: 3, AND TACI
; FILE REFERENCE: 2.001-09-11
; FRIOR PLLING DATE: 2.000-06-12
; PRIOR PLLING DATE: 2.000-06-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 20
; LENGTH: 5.9
                                                                                                                                                         GENERAL INCORMATION:
APPLICANT: THELL, LARS EXDE
APPLICANT: THELL, LARS EXDE
APPLICANT: THELL, LARS EXDE
APPLICANT: THELL, LARS EXDE
APPLICANT: TY, GANG
APPLICANT: TY, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-666B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
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                                                                                                                        Sequence 20, Application US/09854864
Patent No. US20020081296A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Conservative
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US-09-855-158-20
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US-09-854-864-20
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Matches 11; Conserva
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US-09-854-864-16
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JETCH NO. US20020064829A1

JETCH NO. US20020064829A1

JETCH NO. US20020064829A1

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JETCH SPECIAL INFORMATION:

JETCH SPECIAL SPEC
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Pred. No. 2.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | : : | : | : | : | : | : | : | : | 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
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Patent No. US20020160416A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BOYLE, WILLIAM
APPLICANT: HSU, HAILING
ITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
FILE REFERENCE: A-570B
CURRENT APPLICATION NUMBER: US/09/779,050A
CURRENT FILING DATE: 2001-02-12
PRIOR APPLICATION NUMBER: 60/181,800
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 52
SOFTWARE PATENTIN VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                      8; Mismatches
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Pred. No. 4.2;
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          NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 166
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PRIOR FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/21,952
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/211,537
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION UN
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APPLICATION NUMBER: 60/016,812
                                                                                                                                                                                                                                                                                                 33.1%;
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                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 32.4
Matches 11; Conservative
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Best Local Similarity 32.4
Matches 11; Conservative
                                                                                                                                                        TYPE: PRT ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
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LENGTH: 291
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US-09-85-158-15
i Sequence 15, Application US/0985158
i Publication No. US20020086018A1
i GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
ITILE OF INVENTION: ATHORIA TOON
ITILE OF INVENTION: ATHORIA TOON
ITILE OF INVENTION: A. AND TACI
ITILE OF INVENTION OF MATTER CONCERNING APRIL/G70, BCMA, BL
ITILE OF INVENTION NUMBER: US 60/214,591
PRIOR PELING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/204,039
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PARENTIN PARENTING APRIL ASPENDING APPLICATION NUMBER OF SEQ ID NOS: 30
SOFTWARE: PARENTING APPLICATION NUMBER OF SEQ ID NO 15
LENGTH: 166
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TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
FILE REFERENCE: 44158/254623
CURRENT PRILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: US 09/782,857
PRIOR PELLING DATE: 2001-02-14
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
PRIOR FILING DATE: 1999-04-12
PRIOR PILING DATE: 1999-04-12
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33.1%; Score 66.5; DB 9; Length 166;
Best Local Similarity 32.4%; Pred. No. 2.4;
Matches 11; Conservative 8; Mismatches 14; Indels
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 15
LENGTH: 166
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Publication No. US20030082173A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 33.1%;
Best Local Similarity 32.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-855-158-15
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1 Sequence 2, Application US/09961376

2 Sequence 2, Application US/09961376

3 GENERAL INFORMATION:

3 APPLICANT: Ruben et al.

3 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17

3 PILLE REFERENCE: PF524P1

3 CURRENT APPLICATION NUMBER: US/09/961,376

4 CURRENT FILING DATE: 2001-09-25
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                                                                       8; Mismatches 14;
                           DB 9;
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                           Score 66.5; DI
Pred. No. 4.2;
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Pred. No. 4.2;
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Job time : 32.2569 secs
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PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-12-13
PRIOR PILING DATE: 2000-26
PRIOR FILING DATE: 2000-26
PRIOR PILING DATE: 2000-324
PRIOR APPLICATION NUMBER: 60/188, 208
PRIOR APPLICATION NUMBER: 60/188, 208
PRIOR PILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 2
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                        Query Match 33.1%;
Best Local Similarity 32.4%;
Matches 11; Conservative
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Best Local Similarity 32.4
Matches 11; Conservative
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: TU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, ECMA, BI
TITLE OF INVENTION: 3, AND TACI
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-12
PRIOR PILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 14
LENGTH: 293
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APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SSOTUARE: Patentin version 3.1
SSOTUARE: Patentin version 3.1
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Pred. No. 4.2;
8; Mismatches 14; Indels.
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Pred. No. 4.2;
8; Mismatches 14; Indels
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Publication No. US20020086018A1
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Patent No. US20020081296A1
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1 Similarity 32.4%;
11; Conservative
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Best Local Similarity 32.4%;
Matches 11; Conservative
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-879-919-22
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; ORGANISM: Homo sapiens
US-09-854-864-14
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US-09-855-158-14
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DB 2; Length 217;

9.2%; Score 88.5; DB ilarity 24.8%; Pred. No. 0.97; Conservative 25; Mismatches

62 63

SLIHACI PCOLRCSSNTPPLTCORYCNASV-----TINSVKGTNAI----LWTCLGL

-----TGDEIILPRGLEYTVEEC------TCEDCI-KSKPKVDSDH 142

ALIGNMENTS

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A;Cross-references: UNIPROT:097D61; GB:AE001437; PIDN:AAK81542.1; PID:g15026719; GSPDB:GRA;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Weigmann, A.; Corbeil, D.; Hellwig, A.; Huttner, W.B.
Proc. Natl. Acad. Sci. U.S.A. 94, 12425-12430, 1997
A;Title: Prominin, a novel microvilli-specific polytopic membrane protein of the apical & A;Reference number: 216512; MUID:98024147; PMID:9356465
A;Accession: T08881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 SLIISLAVFV--LMFLLRKISSEPLKDEF----KNTGS-----GLLGMANIDLEKSR 108
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08881
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A;Molecule type: mRNA
A;Residues: 1-858 <WEI>
                                                                                                  A;Gene: CAC3619
C;Superfamily: histidine permease protein M
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Best Local Similarity
Matches 55; Conserv
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amino acid ABC transporter, permease component CAC3619 [imported] - Clostridium acetobut c) Species: Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 # acquence_revision 14-Sep-2001 # text_change 09-Jul-2004
C;Accession: C97344
R;Nolling, J.; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J Dally, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
A;Tille: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
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100.0%; Pred. No. 4.1e-81;
live 0; Mismatches 0;
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Best Local Similarity 100.'
Matches 184; Conservative
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A;Cross-references: UNIPROT:054990; EMBL:AF026269; NID:g2559003; PIDN:AAB86715.1; PID:g2!* A;Experimental source: kidney C;Keywords: glycoprotein; membrane protein 10; 78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129 168 GFVANQQTRTRIKGTQK-----LAKSNFRDFQTLLTETPKQIDYVVBQYTNTKNKA 218 130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172 T13009 hypothetical protein T24C20.80 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004 18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 53; Gaps Query Match 9.0%; Score 86.5; DB 2; Length 858; Best Local Similarity 22.7%; Pred. No. 5.9; Matches 44; Conservative 30; Mismatches 67; Indels 5: 173 ---SATEIEKSISA 183 :||: ::||: 272 LQDAATQLNTNLSS 285 RESULT 4 셤 ò

A;Status: preliminary

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protein ROBF11.7 [imported] - Caenorhabditis elegans
C;Species. Caenorhabditis elegans
C;Species. Caenorhabditis elegans
C;Species. Caenorhabditis elegans
C;Accession. D89010
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA*
A;Residues: 1-773 «STO»
A;Cross-references: UNIRROT:001892; GB:chr_V; PIDN:AAB54249.1; PID:g2088832; GSPDB:GN000;
A;Note: Similar to peroxidase
J. Mol. Biol. 222, 835-841, 1991
A/Title: Cysteine residue periodicity is a conserved structural feature of variable surfs
A/Reference number: Z20504; MUID:92106337; PMID:1762150
A/Recession: T28669
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Rotele typelminary; translated from GB/EMBL/DDBJ
A/Rotele typelminary; A/Residues: 1-2233 «NIE>
A/COSS-references: UNIPROT:094711; EMBL:M65164; NID:g159974; PID:g159975; PIDN:AAA61740
A/Genetics: code: SGC5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 IISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDL----EKSRTGDEIILPRGLE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 SSLNCTSC--SSPTTISTNCAPIPAPADDXYFTPVSRTEARCIRLTRALNGQSGFGVRTQ 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 IRNTSVTGSPLPSTRLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSTAKDG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             520 GSCYQKQ-----CSAASQDNTTHAQCQEYLPACTLSNTKKG------CIDLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23 PCQLRCSSNTPPLTCQ-----GLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNA-SVTNSVKGTNAILWTCLGLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 YTVEECTC----EDCIKSKPKVDSDHCFPLPAMEEGATI-----LVTTKTN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 YTVELCEAYKPSSNCV---PNGTKKGCMELAAKCESRTIKEQCDVAGTKTN 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  562 TCSA-----LIVKENCELKANREK---CGWTGSTCVDIVCTTAPTKTDD-
                                                                                                                                                                                                                                                                                                                                         Length 2233;
                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Genetics:
A;Gene: R08F11.7
A;Map position: 5
C;Superfamily: myeloperoxidase; myeloperoxidase homology
                                                                                                                                                                                                                                                                                                                                                                                                        58;
                                                                                                                                                                                                                                                                                                                                            5
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21.7%; Pred. No. 17;
Live 25; Mismatches 91
                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                         Query Match
8.5%; Score 81.5; DB
Best Local Similarity 25.1%; Pred. No. 45;
Matches 43; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 21.77
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177 IEKS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1:::
362 IDQN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - rat
NyAlternate names: cell adhesion kinase-beta
NyAlternate names: cell adhesion kinase-beta
C;Species Rattus norvegicus (Norway rat)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57434
C;Accession: A57434
Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-tyrc
A;Reference number: A57434; MUID:95403356; PMID:7673154
A;Accession: A57434
A;Molecule type: mRNA
                                  Sa
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                                                                                                                                                                                                                                                                                                                                         A;Map position: 3
A;Introns: 71/3; 117/1; 162/3; 230/1; 309/3; 348/2; 396/1; 452/3; 532/2; 604/1; 1005/2;
C;Superfamily: Arabidopsis thaliana hypothetical protein T24C20.80
                                     ъ.
.:
C;Accession: T13009

R;Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, aubmitted to the Protein Sequence Database, July 1999
A;Reference number: Z17586
A;Reference number: Database, July 1999
A;Reference number: Z17586
A;Reference number: L1998
A;Reference number: L1998 <CHO>
                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9STR8; EMBL:AL096856; GSPDB:GN00061; ATSP:T24C20.80
A;Experimental source: cultivar Columbia; BAC clone T24C20
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 GLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP-----KVDSDHCFPLPAM 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   surface protein 51C - Paramecium tetraurelia
C;Species: Paramecium tetraurelia
C;Species: Paramecium tetraurelia
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28669
R;Nielsen, E.; You, Y.; Forney, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 KFFNT---LAGPANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLAEFKQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 QRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKD-EFKN--TGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ERYCSA---NSALGIPSM---C------STGPFQDSEFENFSLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----TGDEIILPRGLEYTVEECTCEDCIKSKPKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.5%; Score 82; DB 2; Length 1009; 26.9%; Pred. No. 18; tive 13; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.7%; Score 83.5; I 29.4%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EFKNTGSGLLGMANIDLEKSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 26.9
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1174 DGGATI 1179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 EEGATI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Residues: 1-1009 <SAS>
                                                                                                                                                                                                                                                                                                               A; Gene: ATSP: T24C20.80
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Ribult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, i. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996

A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C. A;Tile: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii. A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Reference number: A64300; MUID:96337999; PMID:8688087

A;Reference number: A64300; Muid: acid sequence not shown; translation not shown
A;Residues: 1-343 <BUL>
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R;Yamashita, Y.; Pukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohyam, B;Yamashita, Y.; Pukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Ohyam, J. Biochem. 123, 358-368, 1998

A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory re A;Reference number: JC5894; MUID: 98218758; PMID: 9538215

A;Accession: JC5894

A;A
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C;Genetics:
                                                                                                                                                                                                                                                                                                            1150 CSRPLRIDRIANQCVPC----CSERGVTNSTPPTDC-CHCNPENGECINSSVAGKRRIAEW 1205
                                                                                                                                                                                                                                                                                                                                                                                                                           ---FVLMFLLRKISSEPLKDEFKNTGSGLLGMAN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----DSDHCF-PLPAMEEG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72 VLMFL-----NIDLEKSS--EPLKDEFKNTGSGLLGMA------NIDLEKSRTGD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 EYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 potassium channel homolog - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      killer cell inhibitory receptor p91A precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Mar_1998 #sequence_revision 18-Mar-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                   8 CSQNEYFDSLLHACIPCQLRCS----SNTPPLTCQRYCNAS----VTNSVKGTNAIL-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 DYFTALYFSVI-----TITTTGYGDFTPKTFLGRTLTVVYLCVGVGIVMYLFSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
          Length 1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%; Score 78.5; DB 2; Length 343; 20.4%; Pred. No. 13; tive 35; Mismatches 66; Indels 5:
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --VEYSR-----LPRIDVDFTV----LTSCTDQEGPVEYEH 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 IDLEKSRTGDEIILPR-GLEYTVEECTCEDCIKSKPKVDSDH 142
                                                                                                              48;
          2;
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          DB
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8.2%; Score 79.5; D
4.1%; Pred. No. 40;
.ve 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      58 TCLGLS-----LIISLAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        position: REV1308326-1307295
                                                    24.1%;
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es 39; Conservative
                                                                                                              39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:| | ::
200 PNILITAKADE 210
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                                                    Best_Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: D64469
          Query Match
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A;Accession: G02330
A;Status: preliminary
A;Mccession: G02330
A;Status: preliminary
A;Mcule type: mRNA
A;Residues: 1-22, G'. 24-434, L', 436-1009 <8AS>
A;Residues: 1-22, G'. 24-434, L', 736-1009 <8AS>
A;Residues: 1-22, G'. 24-434, T', Tobloka, H'; Kotani, K.; Sasaki, T.
B;Sasaki, H.; Nagura, K.; Ishino, M.; Tobloka, H.; Kotani, K.; Sasaki, T.
J. Biol. Chem. 270, 21206-21219, 1995
A;Title: Cloning and characterization of cell adhesion kinase beta, a novel protein-tyrc
A;Reference number: A57434; MUID:95403356; PMID:7673154
                                    protein-tyrosine kinase (EC 2.7.1.112) CAK-beta - human
NyAlternate names: cell adhesion kinase-beta
Cyspeciaes: Homo sapiens (man)
Cyspeciaes: Homo sapiens (man)
Cyspeciaes: Homo sapiens (man)
Cyspeciaes: Homo sapiens (man)
Cyspeciaes: Homo sapiens
Cyaccession: S60248; G02330; B57434
Cyaccession: S60248; G02330; B57434
Nature 376, 737-745, 1995
A.Tile: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion chann Ayaccession: S60248
A.Fitle: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion chann Ayaccession: S60248
A.Fitle: Protein tyrosine kinase PYK2 involved in Ca(2+)-induced regulation of ion chann Ayaccession: S60248
A.Fitle: Protein type: mRNA
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NyAlternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
NyAlternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin
C;Species: Spedoptera frugiperda (fall armyworm)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43251
R;Cieplik, M;Klenk, H.
submitted to the EMBL Data Library, January 1996
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiper
A;Reference number: Z22368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-1299 <CLE>
A; Residues: 1-1299 <CLE>
A; Cross-references: UNIPROT: Q26489; EMBL: Z68888; NID: g1167859; PID: e219690; PIDN: CAA9311
A; Experimental source: clone Sfurin 6; ovary
C; Function:
A; Description: responsible for the endoproteolytic processing of proproteins with specif C; Keywords: hydrolase; serine proteinase
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A;Residues: 1-22,'G',24-150 <SA2>
A;Cross-references: GB:D45853; NID:g1000676; PIDN:BAA08289.1; PID:d1008884; PID:g1000677
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8.2%; Score 79.5; DB 2;
Best Local Similarity 32.1%; Pred. No. 31;
Matches 25; Conservative 9; Mismatches 29;
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K,Keywords: ATP; phosphotransferase; tyrosine-speci
F;423-686/Domain: protein kinase homology «KID»
F;431-439/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RSIRCLPL --- EEGOAVL 320
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hypothetical protein F2K15.50 - Arabidopsis thaliana ($\text{Species}$: Arabidopsis thaliana (mouse-ear cress) ($\text{Species}$: Arabidopsis thaliana (mouse-ear cress) ($\text{C}$) ate: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 ($\text{C}$) Accession: T45824 ($\text{R}$); Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000 A;Reference number: Z23015 ($\text{A}$)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 112/3; 136/2; 164/3; 237/3; 356/1; 430/1; 460/2; 718/2; 752/3; 781/3; 806/3; A;Note: A_IG002N01.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   770 SSLTDSISGVFGESSDGVSVALGVAAAAGLSVFAFTEDRKQTLKQVDEFLNTKVAPKELV 829
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A;Molecule type: DNA
A;Residues: 1-568 A:SCH>
A;Residues: 1-68 A:SCH>
A;Cross-references: UNIPROT:O04623; EMBL:AF007269; NID:g2191126; PID:g2191152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 ASVTNSVKG----TNAILWTCLGLSLIISLAVFVLM------FLLRKISSEPLK 86
hypothetical protein A_IG002N01.31 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 SILHAC------IPCOLRCSSNTPPLICORYCNASVTNSVKGTNAILWTC--LG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 968;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 PAMEEGATILVTTKTND----YCKSLPAALSATEIEKSISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMAN 101
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A;Experimental source: cultivar Columbia; BAC clone F2K15
C;Genetics:
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                                                                                           C;Accession: T01733
K;Scheet, P.; Maggi, L.
Submitted to the EMBL Data Library, June 1997
A;Description: The sequence of A. thaliana IG002N01.
A;Reference number: 214407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Map position: 3
A;Introns: 69/3; 271/3; 294/1; 327/3; 397/3; 443/3
A;Note: F2K15.50
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Best Local Similarity 21.6%; Pred. No. 45;
Matches 35; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                A, Experimental source: cultivar Columbia
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A,Molecule type: DNA
A,Residues: 1-522 <RIE>
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.(A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Recrease number: A86141; MUID:21016719; PMID:11130712
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C;Genetics:
                                                              cell-surface molecule against cell activa
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C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25; prot
                                                                                                                                                   F)1-23/Domain: signal sequence #status predicted <SIG>
F)24-841/Product: killer cell inhibitory receptor p91A #status predicted <WAT>
F)24-1811/19-220,221:135,316-418,419:517,518-618/Domain: extracellular Ig-like #status F;656-674/Domain: transmembrane #status predicted <TMM>
F)605-776S/Domain: cytoplasmic #status predicted <CYT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                650 AFILFLEFILLERRHRGKFRKDVQKEK-----DLQLSSGAEEPITRKGELQK 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294 CSGDSTCENKLGHPRCNCRSRYELNTTTNTCKPKGNPEY---VEWTTIVLGTTIGF-LVI 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             598 AONSSFYLLSSASAPVELTVSGPIETSTPPPT-----MSMPLGGLHMYLKALIGVSV 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISLAVFVLMFLL--RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRG---- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------LEYTVEECTCEDCIK----SKPKVDSDHCFPLPAMEEGATILVTTKTN 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 RPNPAAATQEESLYASVEDMQTEDGVELNSWTPPEED------PQGET----- 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F16F4.10 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: D86845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQNEYFDSLLHACIPCOLRCS----SNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CSQNEYFDSLL-HACI PCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLII
                                                                                                                                                                                                                                                                                                                                                                                                                       Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                       64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 738;
                                                                                                                                                                                                                                                                                                                                              ch 8.1%; Score 78; DB 2; Length 841;
1 Similarity 22.7%; Pred. No. 35;
46; Conservative 32; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                             A;Cross-references: UNIPROT:08R2Z1; GB:AF040946 C;Comment: This protein function as inhibitory C;Genetics:
A;Map position: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.0%; Score 77.5; C
26.2%; Pred. No. 34;
tive 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYCKSLPAAL-SATEIEKSISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -YAQVKPSRLRKAGHVSPSVMSR 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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   A; Residues: 1-841 <YAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-738 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28;
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C;Species Rattus norvegicus (Norway rat)
C;Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A43353
R;Sheng, Z. 2; Wu, K., Carraway, K.L.; Fregien, N.
B;Sheng, Z. 2; Wu, K., Carraway, K.L.; Fregien, N.
A;Title: Molecular cloning of the transmembrane component of the 13762 mammary adenocarc A;Reference number: A43353; MUID:9235587; PMID:1379596
A;Accession: A43353
A;Accession: A43353
A;Accession: A43353
A;Accession: A43553
A;Accession: A4355
                                                                                                                                                                                                                                                                                                                                          J.Status: preliminary; translated from GB/EMBL/DDBJ
);Molecule type: DNA
|;Molecule type: DNA
|;Molecule type: DNA
|;Molecule type: DNA
|;Molecule type: DNA
|;Cross-references: UniPROT:045251; EMBL:281471; PIDN:CAB03887.1; GSPDB:GN00023; CESP:Cl
|;Experimental source: clone C14B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Map position: 5
A;Introns: 175/1; 209/3; 304/2; 482/3; 611/3; 680/1; 787/1; 1048/3; 1112/2; 1197/2; 1237
C;Superfamily: Caenorhabditis elegans hypothetical protein C14B4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:Z81483; PIDN:CAB03966.1; GSPDB:GN00023; CESP:C14B4.2 A;Experimental source: clone C43D7
                                                                                                              C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T19277; T19909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LOMAGOCSONEYFDSLLH--ACIPCOLRCSSNTPPLTCQRYC----NASVTN-SVKGTNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55 ILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTG----SGLLGMANIDLEKSRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- NASVTNSVKGT
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A;Note: sequence extracted from NCBI backbone (NCBIN:110690, NCBIP:110691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 7.9%; Score 76.5; DB 2; Length 1404; Local Similarity 24.8%; Pred. No. 81; serious 35; Conservative 21; Mismatches 56; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%; Score 76; DB 2; Length 744; Best Local Similarity 22.1%; Pred. No. 47; Matches 34; Conservative 29; Mismatches 57; Indels
                                                                                  - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,Status: preliminary; translated from GB/EMBL/DDBJ,Molecule type: DNA
,Residues: 1-1404 <WI2>
                                                                                                                                                                                                                  R;Basham, V. submitted to the EMBL Data Library, November 1996 A;Reference number: Z19100 A;Reference number: Z19277 A;Accession: T19277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Basham, V. ubmitted to the EMBL Data Library, November 1996; Recession: T19909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ascites sialoglycoprotein-2 - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 DEILLPRGLEYTVEECTCEDC 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 TIFV-----KYSMNIVLHEDC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Keywords: glycoprotein
F; 655-694/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q63661
                                                                                  ypothetical protein C14B4.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 1-744 <SHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP:C14B4.2
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      C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72288
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                            Aguare 399, 323-329, 1999
Ajtitle: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A; Reference number: A72200; MUID:99287316; PMID:10360571
A; Accession: F72288
A; Accession: F72288
A; Status: preliminary
A; Molecule type: DNA
A; Residuae: 1-539 cARN-
A; A; Cross-references: UNIPROT:09X0N0; GB:AE001772; GB:AE000512; NID:94981693; PIDN:AAD3622
A; Experimental source: strain NSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A,Residues: 1-357 <WIL>
A,Cross-references: UNIPROT:Q9XV87; EMBL:281508; PIDN:CAB04138.1; GSFDB:GN00023; CESP:FZ
A,Experimental source: clone F20E11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 LGMANIDLEKSRT-GDEIIL--PRG----LEYTVEECTCEDCIKS-----KPKVDSDHC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             42 NASVĮNSVKGINAILWICLGLSLIISLAVFVLMFLLRKISSEPLKD---EFKNTGSGLLG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 ACIPCQLRCSSNTPPLTCQRYCNAS-----VTNSVKGTNAILWTCLGLSLIISLAVF 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 VLMF-----EFKNTGSGL 96
Species: Thermotoga maritima
Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F20E11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Aate: 15-061-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T21152
R;Ainscough, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19383
A;Accession: T21152
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Introns: 52/3; 88/2; 103/3; 154/3; 190/2; 205/3; 241/2; 270/3; 321/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.0%; Score 77; DB 2; Length 539; Best Local Similarity 32.0%; Pred. No. 28; Matches 24; Conservative 19; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: TM1146
C;Superfamily: methyl-accepting chemotaxis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.9%; Score 76.5; D. Best Local Similarity 21.7%; Pred. No. 20; Matches 45; Conservative 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -- FPLPAMEEGATILVTTKTNDYCKSL 168
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A;Gene: CESP:F20E11.7
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Cidecies Clostridium acetobutylicum Cipecies Clostridium acetobutylicum Cipecies Clostridium acetobutylicum Cipecies Clostridium acetobutylicum Cipecies Clostridium acetobutylicum CiDate: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004 CiAccession: B97297
Rivolling, J.; Bractci, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J. Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clos A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97297
A;Accession: B97297
A;Accession: By7297
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A;Experimental source: Clostridium acetobutylicum ATCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Brassica oleracea (wild cabbage)
C;Species: Brassica oleracea (wild cabbage)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 11-Jun-1999
C;Accession: A41369
R;Stein, J.C.; Howlett, B.; Boyes, D.C.; Nasrallah, M.E.; Nasrallah, J.B.
Proc. Natl. Acad. Sci. U.S.A. 88, 8816-8820, 1991
A;Title: Molecular cloning of a putative receptor protein kinase gene encoded at the self A;Reference number: A41369; MUID: 92020942; PMID: 1681543
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                                                                                                                                                                                                                                                                                                        ----TCEDCIKSKPKVDSDHCFPLPAMEEGATILVT 158
                                                                                                                                                                                                                                                                                                                                               135 AKLKFGPVNSVQFNDAYSTHISPKLPGRAYEDC----QKFEIDNPSLSPVDKHGAIILRT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 DNIVEKIKECDSSCHSNEGETPCQKSCPFDAILVDKNTKTSHIQKDLCTDCGNCITSCPS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 LSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMA------NIDLEKSRT--- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----VEECTCEDCIKSKPKVDSD---HC 143
                                                                                                                                                                                                                                     89 L-----PNSRPYLSERVRKHTHL-----LSNSITGDDKPSLIHVDFTPEECFILQE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 KVGFADMVEVAFFADMLTIKEAFEFNELVNSKDDLMITSCCCPMWVSMIRKIYKDLARHV 241
                                                                          .----LWTCLG 61
                                   7
                                   EYPDSLIHACI PCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLGLSLIISLAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68; Gaps
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A;Molcoule type: DNA
A;Residues: 1-857 <5TE>
A;Cross-references: GB:M76647; NID:g167166; PIDN:AAA33000.1; PID:g167167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nydrogenase chain (ferredoxin) [imported] - Clostridium acetobutylicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 450;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 DSLLHACIPCQLRCSSNTPPLTCQRYC--NASVTNSVKGTNAI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.8%; Score 75; DB 2;
Best Local Similarity 20.5%; Pred. No. 35;
Matches 42; Conservative 23; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GDEIILPRGLEYT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 SPSVSPMIASGRVI---KKLNPNCK 263
                                                                                                                                                                                                                                                                                                                                                                                                                                           159 TKTN-----DYCKS 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 YKKNKKLLPDYLKS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-450 <KUR>
                                                                                                                                                                                                                                                                                                        127 -----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CAC3230
                                   12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Neurospora crassa
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47250
R;Kuffner, R.; Rohr, A.; Schmiede, A.; Krull, C.; Schulte, U.
A. Mol. Biol. 283, 409-17, 1998
A;Title: Involvement of two novel chaperones in the assembly of mitochondrial NADH:Ubiqu
A;Reference number: Z22191; MUID:9769214; PMID:9769214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: required for complex I membrane arm assembly
C; Superfamily: Neurospora crassa complex I intermediate-associated protein CIA84
C; Keywords: mitochondrion
F; L-C01 Domain: transit peptide (mitochondrion) #status predicted <TNP>
F; L-C01 Domain: transit peptide (mitochondrion) #status predicted <MAT
                                                                                                                                                                                                                                                                                                                                                                                                                                              complex I intermediate-associated protein CIA84 precursor, mitochondrial [imported] - Ne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:O74910; EMBL:AL031644; PIDN:CAA21064.1; GSPDB:GN00068; SPDB:
A;Experimental source: strain 972h-; cosmid c613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Map position: 3;Schizosaccharomyces pombe probable transcription regulator SPCC613.12c;Superfamily: Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
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                                                                                                         82 SEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSD 141
   49 LEGRTAQTDSANATNFIAFAAQYNTSSLKSPITVQWFLEPNDTIRVVHNNQTVAFNTSDT 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       266 SKPIHSGPSPTGETLLELVRSSRRSSQKWNEWLLP-----VFEQVVQDKFAKKGSLDAF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41479
R;Bothe, G.; Pohl, T.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
Bubmitted to the EMBL Data Library, September 1999
A;Reference number: Z21997
A;Accession: T41478
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-638 <BOTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transcription regulator - fission yeast (Schizosaccharomyces pombe)
                                                                      ----ISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 HCFPLPAMEEG----ATILVTTKTNDYCKSLPAALSATEIEKSISA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.9%; Score 76; DB 2; Length 748; Best Local Similarity 25.5%; Pred. No. 47; Matches 27; Conservative 20; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 47;
20; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                                   167 VWNDNPE-----DDFRMPNG--STIPSNTSEETL 193
                                                                                                                                                                                                         99 MANIDLEKSRIGDEIILPRGLEYTVEECTCEDCI 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: T47250
A,Status: prellminary: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-748 «KUE»
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                                                                   53 NAI-LWTCLGLSLI---
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Best Local Similarity 22.79
Matches 44; Conservative
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C; Function:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: 1-1101 <GEI>
A;Residues: 1-1101 <GEI>
A;Cross-references: UNIPROT:022378; EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA8038
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chitinase (EC 3.2.1.14) 35 - Streptomyces thermoviolaceus
Cispecies: Streptomyces thermoviolaceus
Cipate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 09-Jul-2004
CiAccession: JC7535
R;Tsujibo, H.; Okamoto, T.; Hatano, N.; Miyamoto, K.; Watanabe, T.; Mitsutomi, M.; Inamol Biosci. Biotechnol. Biochem. 64, 2445-2453, 2000
A;Title: Family 19 chitinases from Streptomyces thermoviolaceus OPC-520: Molecular clonin. A;Reference number: JC7535; MUID:21036907; PMID:11193414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:Q9RHU5; DDBJ:AB016842
A;Experimental source: strain OPC-520
C;Comment: This enzyme, a member of the family 19 chitinases, is involved in chitin degra
lysaccharide-binding domain that is important in the efficient hydrolysis of insoluble ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C;Accession: B9:5099
R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
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                                                                                                                              C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 NSANGTRVQIWTCTGGSNQKWNAPATGGGSTPAPSGFVVSEAQFNQMFPNRNPFYTYQGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 OCSONEYPDSLIHACIPCOLR -- CSSNIPPLICORYCNASVINSVKGIN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%; Score 74.5; DB 2; Length 1101; 36.7%; Pred. No. 96; tive 11; Mismatches 15; Indels 5
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                                                                                                                                                                                                                                           R'Geisel, C. submitted to the EMBL Data Library, October 1995 A, Description: The sequence of C. elegans cosmid T10E10. A, Reference number: Z18588
                                                                                                                hypothetical protein T10E10.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 NSVKGTNAILWTCLGLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
ses 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: JC7535
A;Molecule type: DNA
A;Residues: 1-377 <TSU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: CESP:T10E10.4
                                                                                                                                                                                                                                                                                                                                                                             A; Accession: T16840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: chi35
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Matches
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Matches
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A; Experimental source: S6S6 homozygote kale
C; Genetics:
A; Gene: SRK
A; Note: SRK
A; Note: SRK
A; Note: SRK
A; Note: Iocus is highly polymorphic
C; Function:
A; Description: involved in preventing fertilization between plants having the same S-loc
C; Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprotein
C; Keywords: ATP; glycoprotein; magnesium; phosphotransferase; receptor; serine/threonine
F; 1-30/Domain: signal sequence #status predicted <SIG>F; 31-857/Product: S-receptor kinase #status predicted <NAT>F; 447-466/Domain: transmembrane #status predicted <TWM>F; 524-813/Domain: protein kinase homology <KIN>F; 524-813/Domain: protein kinase ATP-binding motif
F; 534-542/Region: protein kinase ATP-binding motif
F; 571-120, 196, 260, 314, 389, 442/Binding site: carbohydrate (Asn) (covalent) #status predict
F; 558, 652/Binding site: magnesium (Asn, Asp) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P41771; EMBL:U04714; NID:g436876; PIDN:AAA21530.1; PID:g4368 A;Note: the source is designated as Kluyveromyces lactis C;Genetics: A;Gene: ERD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               435 ADIAKKRNASGKIISLTVGVSVLLLLIMFCL-----WRRKOKRAKASAISIANTORNO 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSLKLFKSISRVIIPWQLVC-----ILLFQY---SFTNNV--SNKLLWFFLNVSPLLEL 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 -------CLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 SRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCF-----PLPAMEEGATILVTTKT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69 AVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERDI protein - yeast (Kluyveromyces marxianus var. lactis)
C;Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
C;Daces: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: 845592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yeast 10, 1117-1124, 1994
A/TILLs: Cloning and DNA sequence of a Kluyveromyces lactis ERD1 homologue.
A/Reference number: 845592; MUID:95084639; PMID:7992512
A/Accession: 845592.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 EDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----SKPLVD-----LAIYATFLFHDPTNVKCQ 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 COLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.8%; Score 75; DB 1
Best Local Similarity 17.6%; Pred. No. 67;
Matches 33; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.7%; Score 74.5; D
llarity 27.2%; Pred. No. 33;
Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 NDYCKSL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            528 FSSCNKL 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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A;Residues: 1-384 <DEA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43;
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Best Local S
Matches 43
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셤 ò 유 ò

ò 셤 ò 임 ò 유 ò 8

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C;Accession: A89882
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguci M.; A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; E.; Sahiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:099UY7; GB:BA000018; PID:gl3700917; PIDN:BAB42213.1; GSPDB:G:
A;Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Directing F20N2.12 [imported] - Arabidopsis thaliana protein F20N2.12 [imported] - Arabidopsis thaliana (mouse-ear cress)
CjSpecies: Arabidopsis thaliana (mouse-ear cress)
CjSpecies: Arabidopsis thaliana (mouse-ear cress)
CjAccession: B96599
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, I A;Feference and analysis of chromosome in of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:Q9ZWD7; GB:AE005173; NID:g8778489; PIDN:AAF79497.1; GSPDB:GN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 LIMGGACALMNYYDQDIDRIMPSK----QNRP-----TVNNRITDQNLLLLS-FG 111
                                                                                                                                                                                                     C.Species: Staphylococcus aureus
C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 LOMAGOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLG
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                                                                                                                                                                        hypothetical protein ctaB [imported] - Staphylococcus aureus (strain N315)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Length 304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----NIPSGVLGLMGI 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 LSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.6%; Score 73; DB 2
Best Local Similarity 23.8%; Pred. No. 36;
Matches 24; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.6%; Score 73; DB
llarity 22.2%; Pred. No. 81;
Conservative 21; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: ctaB
C;Superfamily: heme O synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : |: : : |: |
112 MMLVGEICLFLL---
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les 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-304 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Molecule type: DNA
A, Residues: 1-679 <STO>
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                147 KSL 149
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Matches
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP0859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q97RG2; UNIPROT:Q8DQB0; GB:AE007317; PIDN:AAK99565.1; PID:g1
C;Genetics:
A;Gene: spr0761
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95099
A;Accession: E95099
A;Accession: Lype: DNA
A;Refelence type: DNA
A;Residues: 1-307 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 27
A97967
conserved hypothetical protein spr0761 [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
R;Hoskins, J.A.; Abborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M. P., Sun, P.M.; Winkleber, M.B.
J. Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Acteriol. Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Acteriol. Dyniminary
A;Acteriol. Dyniminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 KSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYC 165
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                                                                                                                                                                                                                                                                                                                                                                                                                               7.6%; Score 73.5; DB 2; Length 307; 26.2%; Pred. No. 33;
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Best Local Similarity 26.2%
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.23
Matches 48; Conservative
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A; Residues: 1-307 < KUR>
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Gaps

32;

Indels

61

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44; Gaps

Length 679; Indels

protein

7;

74

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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N.
w.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umayam, L.; Tallon, L.:
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
Affile: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Synechocystis sp.
A; Variety: PCC 6803
C; Date: Date: 1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: S75097
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                       A;Cross-references: UNIPROT:085853; EMBL:AF079317; NID:g3378261; PID:g3378285; PIDN:AADO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein At2g14520 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: B84518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AVEYECCGTSFFIHIAVIVLLVLFAGLMS-----GITLGLMSMSLVDLEVLAKSGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LHACIPC - QLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -------BLLRKISSEPLKDEFKNTGS-----GLLGMANIDLEKSRTGDEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143 IPALDWETHAGATNPDVRPASGAFGCQECRDTGARCDQPPGPIGLIADDIEND---
                                                                                                                                                                                                                                                                 A;Note: orf171
C;Superfamily: Sphingomonas aromaticivorans plasmid pNL1 hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 -PRDPB-TEGASLGDDCLRASVAVEVLHLLDRSRRIACRAGVFAFAPLPA 243
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                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 243;
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                                             translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 DEILLPRGLEYTVEECTCEDCIKSKPKVDSDH 142
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                                                                                                                                                                                                                                                                                                                                                                       7.5%; Score 72.5; Dilarity 22.9%; Pred. No. 32; Conservative 22; Mismatches
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Best Local Similarity 29.3%; Pred. No. 54;
Matches 27; Conservative 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
.....hes 39; Conserva
                                                                                                                 A; Residues: 1-243 < ROM>
                                             A;Status: preliminary;
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A; Residues: 1-408 <STO>
                                                                                                                                                                                                                           A; Genome: plasmid pNL1
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                                                                               A, Molecule type: DNA
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A;Map position: 2
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                                                                                                                                                                                                                                                                                                                                                        probable serine/threonine-specific protein kinase (EC 2.7.1.-) PRO25 - Arabidopsis thaliprobable serine/threonine-specific protein kinase (EC 2.7.1.-) PRO25 - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 19-Jul-2002 #text_change 09-Jul-2004
C;Accession: H86345; A46373
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudghes, B.; Huizar, L.
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A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roomey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vencer, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86345
A;Accession: H86345
A;Accession: H86345
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MResidues: 1-733 <cstro.
A,Residues: 1-733 <cstro.
A,Stesidues: 1-733 <cstro.
A,Strosidues: 1-733 <cstro.
A,Cross-references: UNIPROT: O91MPO; GB:AE005172; NID:g8920634; PIDN:AAF81356.1; GSPDB:GN
R,Kohorn, B.D.; Lane, S.; Smith, T.A.
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A,Stoc. Natl. Acad. Sci. U.S.A. 89, 10898-10892, 1992
A,Title: An Arabidopsis serine/threonine kinase homologue with an epidermal growth factch.
A,Reference number: A46373; MUID:93066369; PMID:1438303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: mRNA
A,Residues: 138-211, 'C',213-243,'I',245-279,'CQD',281-384,387-455,'P',457-660,'T','N',66
A;Cross-references: GB:L04999; NID:g166812; PIDN.AAA2844.1; PID:g166813
A;Note: sequence extracted from NCBI backbone (NCBIN:118788; NCBIP:118790)
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hypothetical protein 171 - Sphingomonas aromaticivorans plasmid pNL1

hypothetical protein 171 - Sphingomonas aromaticivorans

hypothetical protein 171 - Sphingomonas aromaticivorans

C; Species : Spinimgomonas aromaticivorans

C; Bate: 11-3an-2000 #sequence_revision 11-3an-2000 #text_change 09-Jul-2004

C; Accession: T31144

E; Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G

submitted to the EMBL Data Library, July 1998

A; Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromati

A; Reference number: Z20992
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C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25;
C;Keywords: phosphotransferase
                                     ---SLPŠĠ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 CRCNEGFDGNPYLSAGYVNECTTSSTIHRHNCSDPKTCRNKVGGFYCKCQSGYRLDTTTM 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
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257 GLSLEN----TNDYVYACLSCNLMVHMACIFLPRVIKITRHQHRLSLSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 7.6%; Score 73; DB 1; Length 733; Best Local Similarity 23.3%; Pred. No. 88; Matches 37; Conservative 27; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :|:| : | : | : | | SGAGPSNVDVKIFTEDGMKKATNGYAESRILGQGGQGTV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---GMANID-----LEKSRIG--DEIILPRGLEYTV 123
                                                                                                                                                              307 IYPCGVCRLTIDVTYGOFSCNRGCHYAVHSKCAIEERI
                                                                                                             96 LLGMANIDLEKSRTGDEIILPRGLEYTV-EECTCEDCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;405-684/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Accession: A46373
A;Status: preliminary
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A;Cross-references: UNIPROT:092EC6; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA1448! A;Experimental source: strain Madrid E
C;Genetics:
A;Gene: RP017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 399, 323-329, 1999
A;Title: Bvidence for lateral gene transfer between Archaea and Bacteria from genome seqn
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: F72334
            R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.
kirology 259, 381-339, 1997
A;Title: The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis
A;Reference number: Z17011; MUID:97271300; PMID:9126251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: B71709
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
A;Accession: B71709
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hiq
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 NSSLNDCIN-QLRC-ANTSDVYNLSYTLSNKTKQLSIDELKNTLEQMQTSPNINIVLPML 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : | : : : : | | : : : : | 376 IRVQQDYVNEVAEIYQQTIEQRKQNPSEQAKNQEEVVAAYFTQEYDKLKIINSFRSLKTD 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 --TGSGLLGMANI-----DLEKSRTGDEIILPRGLEYTVE-EC-TCEDCIKSK-PKVDSD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          436 SITNTSLASSVNIFGSNEDLSWDNTGD---IGVGYRYGPEHSCPTPDDRLSSKLIDMSNK 492
                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-105 -AHR>,
A)Cross-references: EMBL: U75930; NID:g2934903; PIDN:AAC59080.1; PID:g1911327
C;Superfamily: uncharacterized conserved protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Decies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: F72334
R;Nelson, K.B.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodgon, R.J.; Haft,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein RP017 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 DSLLHACIPCOLRCSSNTPPLTCORYCNASVT----NSVKGTNAILWTCLGLSLIISLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 VFVLMFLLRKIS-----FKN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HINTRINGLEEGVTIYDSIDSVADPLKSNDVSFEEINEALKOLSAAISETVINSSES 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 HCFPLPAMEEGATILVT-----TKTNDY------CKSLPAALSATEIEKSIS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22 IPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.4%; Score 71.5; DB 2; Length 627; Best Local Similarity 22.9%; Pred. No. 1e+02; Matches 54; Conservative 36; Mismatches 73; Indels 7.
                                                                                                                                                                                                                                                                                                                                             Length 105;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                            30;
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                                                                                                                                    A, Accession: T10350
A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                   8; Mismatches
                                                                                                                                                                                                                                                                                                                                             Score 71.5; I
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 30.4%;
Matches 17; Conservative 6
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A; Residues: 1-627 < AND>
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A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75097
A;Status: preliminary
A;Molacule type: DNA
A;Residues: 1-416 «KMN*
A;Cross-references: UNIPROT:P73895; EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA1795
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: Synechocystis hypothetical protein s110243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T10665
**Sevan. M.; Lennard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancrd Bubmitted to the Protein Sequence Database, June 1999
A;Reference number: Z16533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prot
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A;Introns: 345/1; 756/2
C;Superfamily: Arabidopsis probable serine/threonine-specific protein kinase PRO25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A;Residues: 1-855 <BEV>
A;Cross-references: UNIPROT:Q9M091; EMBL:AL049914; GSPDB:GN00062; ATSP:F6E21.30
A;Experimental source: cultivar Columbia; BAC clone F6E21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- KPQ 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 SRIQYASLILHQPVPLSISIEDLLQAYDNVTEYEDQRYLFWSIIHFLPQELQTIDQSTFL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 NTIKRLTQRQLIESDGDKIAWTESGLFLISSLHRRLCILAIDLLGYNETNLLGRQGALLI 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KISSEPLKDEFKNTGSGLLGMANIDLEKS-RTGDEIILPRGLEYTVEECTCEDCIKSKPK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F6E21.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTSNRSFLDSLALACKDREDYRNTTNLERKCTCGRITISETSYANCGCTYGYTGNPYVLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSVK-----GTNAILWTCLGLSLIIS-----LAVFVLMF-----LLR
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                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                 88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VD-----SDHCFPLPAMEEGATILVTTKTNDYCKSLPAAL 172
                                                                                                                                                                                                                                                                                  Query Match 7.5%; Score 72; DB 2; Length 416; Best Local Similarity 21.2%; Pred. No. 61; Matches 48; Conservative 30; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 855;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           287 RAENSLWFFDIDPSPNGLVSVVSISLDKAYELLDEIFTPVG-
                                                                                                                                                                                                                                                                                                                                                                                                         SQNEYFDSLLHACIPCQ-----LRCSSNTPPLTCQRYC-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 21.5
Les 37; Conservative
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A;Gene: ATSP:F6E21.30
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Best Local S:
Matches 37,
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T10350
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Best Local Similarity 21.11
Matches 35; Conservative
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A;Residues: 1-480 <STO>
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ABC transporters (permease protein) homolog lmol062 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AF1207
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable cell division protein (ftsA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Bacession: G71331

R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwir seno, U.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDc they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:965876
A;Accession: G71331
A;Resion: G71331
A;Residues; 1-414 <COL>
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A;Genetics
A;Genetics: TP0389
C;Superfamily: cell division protein ftsA
                                A;Molecule type: DNA_A;Residues: 1-227 <ARN>A;Residues: 1-227 <ARN>A;Residues: 1-227 <ARN>A;Residues: 1-227 <ARN>A;Residues: UNIPROT:Q9WZQ4; GB:AE001747; GB:AE000512; NID:g4981304; PIDN:AAD3587 A;Experimental source: strain MSB8 C;Genetics: A;Genetics: A;Gene: TM0797 C;Superfamily: Synechocystis hypothetical protein slr1718
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84 PLKDEFKNTGSGL--LGMANIDLEKSRTGDEIILPR----GLEYT-----VEECTCEDCI 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEE 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 ASVTINSVKGTNAILWTCLGLSLIISLAVFVLM-FLLRKISSEPLKD-
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A;Status: preliminary
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D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
A;Authors: Kreft, J.; Kunn, M.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUD:21537279; PMID:11679669
A;Sccession: AF1207
A;Status: preliminary
A;Status: preliminary
A;Status: DNA
A;Residues: 1-473 <GLA>
                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8Y856; GB:NC_003210; PIDN:CAC99140.1; PID:g16410464; GSPDB:CA;Experimental source: strain EGD-e
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R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology.
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/ A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: G88690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 EKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKVDS------DHCFPLPAMEE-- 151
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C.Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
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------EDCLET 208
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Best Local Similarity 24.6%; Pred. No. 86;
Matches 33; Conservative 28; Mismatches
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Query Match
Best Local Similarity
Matches 27; Conserv
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            A;Residues: 1-188 <GLA>
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A,Title: Adelaide river rhabdovirus expresses consecutive glycoprotein genes as polycist
A,Reference number: Z14732; MUID:93331730; PMID:8337841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Residues: 1-660 <WAN>
A,Cross-references: UNIPROT:Q89669; EMBL:L09206; NID:g348027; PIDN:AAA02762.1; PID:g3486
A,Experimental source: isolate DPP61
C,Superfamily: rhabdovirus spike glycoprotein G
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H82933
C;Pecies Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: H82933
E;Glass, J.1.; Glass, J.S.; Heiner, C.R.; Chen, B.Y.; Cassell, G.H. submitted to GenBank, Pebruary 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
                                                                                                               G.; Ba
hypothetical protein F313.50 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C; Accession: T10543 Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volckaert, R; Bevan, M.; Robben, J.; Volckaert, Bubmitted to the Protein Sequence Database, June 1999
A; Reference number: 217080
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                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q9SV26; EMBL:AL080237; GSPDB:GN00062; ATSP:F313.50
A;Experimental source: cultivar Columbia; BAC clone F313
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : : : | | : | : | | : | | HOYAMFGRGEEGIAAFSVML---EAGMEPDAITFISVLSVCKNSGLVQEGWKYFDLMRSR 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SILHSGKEVHGFCLRKNLICDAYVATALVDMYGKSGDLQSAIBIFWGIKNKSLASWNCML 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 LSLII-----SLAVFVLMFLLRKISSEPLKDEF-----KNTGSGLLGMANIDLEKSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          spike glycoprotein G homolog - Adelaide River virus
C;Species: Adelaide River virus
C;Date: 23- Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T02768
R;Wang, Y;; Walker, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLIMA-----VKGTNAILWTCLG
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.4%; Score 71; DB 2; Length 500; Best Local Similarity 23.6%; Pred. No. 91; Matches 33; Conservative 17; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 7.4%; Score 71; DB 2; Length 660; Local Similarity 32.7%; Pred. No. 1.2e+02; es 18; Conservative 13; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 TGDEIILPRGLEYTVEECTC 128
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: genomic RNA
                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-500 <BEV>
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Best Local &
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A;Cross-references: GB:AE002110; GB:AF222894; NID:g6899051; PIDN:AAF30507.1; GSFDB:GN001: A;Experimental source: serovar 3; biovar 1 GGenteios: GGenteios: A;Genteios: A;Genteios: U1001
A;Gene: U1001
A;Gene: Code: SGC3
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A;Experimental source: clone R07B7
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Proc. Natl. Acad. Sci. U.S.A. 94, 7673-7678, 1997
A,Title: Striking sequence similarity in inter- and intra-specific comparisons of class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                      51 GTNAILWTCLGLSLIISLAVFV---LMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKS 107
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                                                                                                                                                                                                                                                                                                                                                                                                           35.GDEAYKTSDLGSELYINYADPESTNILFDLKKEELQAKIDAFLISNDTVLDLSEVFLDIH 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein R07B7.16 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 16-Aug-2004
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C;Species: Barasica oleracea (wild cabbage)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14525
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                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                           Length 188;
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                                                                                                                                                                                                                                                                                                 39;
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                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Introns: 26/3; 53/3; 89/1; 139/3; 203/2; 325/1
C;Superfamily: erbA transforming protein homology
                                                                                                                                                                                                                       7.3%; Score 70.5; Dilarity 25.5%; Pred. No. 37; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Harris, B.
submitted to the EMBL Data Library, July 1996
A;Reference number: Z19830
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39; Gaps

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hypothetical protein F2401.2 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Acression: T01440
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; Conway, A.; Eker, J.R.
submitted to the EMBL Data Library, January 1998
A;Description: Genomic sequence for Arabidopsis thaliana BAC F2401.
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A;Cross-references: UNIPROT:048794; EMBL:AC003113; NID:92689438; PID:92781345; GSPDB:GNOC
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R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 cot A;Reference number: A42916; MUID:92317054; PMID:1320017
                                        EMBL:X83758; NID:g790481; PID:g790482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 211 QCLKGERITLLI -- CSECEKTWFCLQCIRKWYPNLSEDDVVEKCPLCRONCNCS---- 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---DLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPKV--DSD 141
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metabotropic glutamate receptor mGluR5 - rat
C:Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 TCQRYCNASVINSVKGTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNT-GS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 HCFPLPAMEEGATI---------LVTTKTNDYCKSLPAALSA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 906;
                                                                                                                                                                                                                                                             Length 839;
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A;Introns: 239/2; 272/3; 317/1; 338/2; 682/3; 832/1; 860/3
                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                       Query Match 7.3%; Score 70.5; DB 2; Best Local Similarity 21.6%; Pred. No. 1.7e+02; Matches 37; Conservative 26; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 7.3%; Score 70.5; DB 2; Local Similarity 20.9%; Pred. No. 1.8e+02; Nes 37; Conservative 19; Mismatches 54;
                                        A;Cross-references: UNIPROT:Q26024; UNIPROT:Q81329;
C;Superfamily: eukaryotic type I DNA topoisomerase
C;Keywords: DNA binding; DNA replication; isomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: T01440
A;Status: translated from GB/EMBL/DDBJ
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A;Residues: 1-839 <TOS>
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Best Local S
Matches 37
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                                  A; Accession: T14525
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-treferences: UNIPROT: 023834; EMBL: D85200; NID: 92351131; PIDN: BAA21934.1; PID: 9235
C; Superfamily: S-locus-specific glycoprotein; S-locus-specific glycoprotein homology
C; Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        554174

DNA topoisomerase (BC 5.99.1.2) - malaria parasite (Plasmodium falciparum)

C;Species 1 lasmodium falciparum

C;Date: 08-Uul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C;Accession: S54174

R;Tosh, K.T.; Kilbey, B.J.K.

Submittion: Loolation and characterisation of the topoimerase 1 gene from Plasmodium A;Reference number: S54174

A;Accession: S54174

A;Accession: S54174

A;Referus: preliminary

A;Molecule type: DNA
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A)Residues: 1-490 < DAN>
A)Cross-references: EMBL:AF016668; PIDN:AAB66095.1; GSPDB:GN00020; CESP:F36H9.4
A)Experimental source: strain Bristol N2; clone F36H9
C)Genetics:
A)Genetics:
A)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F36H9.4 - Caenorhabditis elegans
hypothetical protein F36H9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T32003
R;Danne, M; Kramer, J; Twyman, B.
A;Danne, M; Kramer, J; Twyman, B.
A;Description: The sequence of C. elegans cosmid F36H9.
A;Accession: T32003
A;Accession: T32003
A;Accession: T32003
A;Accession: T32003
A;Accession: T32003
A;Accession: T32003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 424;
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A; Reference number: Z18078; MUID: 97352858; PMID: 9207151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 CQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWT 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 7.3%; Score 70.5; I Best Local Similarity 40.0%; Pred. No. 85; Matches 14; Conservative 5; Mismatches
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A;Status: preliminary A;Molecule type: mRNA

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A; Cross-references: UNIPROT: P31424; GB: D10891; NID: 9220813; PIDN: BAA01711.1; PID: d100216

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1548 <NMX>
A;Cross-references: UNIPROT:Q04592; GB:D17583; NID:g407344; PIDN:BAAQ4507.1; PID:d100503
C;Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S34583
R;Nakagawa, T.; Murakami, K.; Nakayama, K.
EBBS Lett. 327, 165-171, 1993
A;Title: 1dentification of an isoform with an extremely large Cys-rich region of PC6, a A;Reference number: S34583; MUID:93327934; PMID:8335106
A;Accession: S34583
                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                          62 LSLIISLAVFVLMFLLR-----KISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                    117 RGLEYTVEEC---TCEDCIKSKPKVDSDHCF-----PLPAMEEGATILVTTKTN---- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |-----CLGYLCTFCLIAKPK--QIYCYLQRIGIGLSPAMSYSALV---TKTNRIAR 670
                                                                                                                                                                                                                                                                                                                                                                                  -----YIIL 621
                                                                                                                                                                                                                   8 CSQNEY-FDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTN-----AILWTCLG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                serine proteinase (EC 3.4.21.-) PC6B - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
A, Experimental source: brain
A, Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBIP:107750)
C, Keywords: G protein-coupled receptor; transmembrane protein
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                                                                                                         Query Match 7.3%; Score 70.5; DB 2; Length 1171; Best Local Similarity 24.6%; Pred. No. 2.4e+02; Matches 49; Conservative 21; Mismatches 52; Indels 77
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5; Mismatches 22; Indels 5;
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ALIGNMENTS

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EMBL;
Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; NINEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)."; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.

MEDLINE-20363816; PubMed=10903733;

Hatzoglou A., Roussel J., Bourgade M.-F., Rogier E., Madry C.,

Inoue J.-I., Devergen C., Taspis A.,

"TNF receptor family member BCMA (B cell maturation) associates with

TNF receptor resocciated factor (TRAF) 1, TRAF2, and TRAF3 and

activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38 mitogen-

activated protein kinase.;

J. Immunol. 165:1322-1330(2000).
                                                                                                                                                                                                                                                              Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
Larsen C.J., Tsapis A.;
"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
by a t(4;16) (q26;p13) translocation in a malignant T cell lymphoma.";
EMBO J. 11:3897-3904 (1992).
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=94218235; PubMed=8165126;
Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
"The BCMA gene, preferentially expressed during B lymphoid maturation,
is bidirectionally transcribed.";
Nucleic Acids Res. 22:1147-1154(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=99425270; PubMed=10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R.,
Enthrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L.,
Dealattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S.,
Eichlar B.E., Harris P.C., Venter J.C., Adams M.D.;
"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND VARIANTS VAL-54; VAL-65; VAL-75; ASN-81 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT THR-153.
MEDILINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770;
Kawasaki A., Tsuchiya N., Fukazawa T., Hashimuco H., Tokunaga K.;
"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20259066; PubMed=10801128; DOI=10.1038/35010115;
Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
Madden K., Xu W., Parrish-Novak J., Foster D., Lofton-Day C.,
                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.
TISSUE=Lymph node, and Peripheral blood leukocytes;
MEDLINE=93010984; PubMed=1396583;
                                       184 AA
                                                                                                                      maturation protein).
Name=TNFRSF17; Synonyms=BCMA, BCM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis.";
Jenes Immun. 2:276-279(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genomics 60:295-308(1999),
                                   STANDARD;
                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                           NCBI_TaxID=9606;
                    7 HUMAN
TR17 HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERACTIONS WITH TRAFF AND TRAFG.

MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;

MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;

Shu H.-B., Johnson H.;

"B call maturation protein is a receptor for the tumor necrosis factor family member TALL-1.";

Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).

-I- FUNCTION: Receptor for TNFSP13B/BLyS/BAFF and TNFSP13/APRIL.

Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and JNK.

-I- SUBUNIT: Associates with TRAPI, TRAF2, TRAF3, TRAF5 and TRAF6.

-I- SUBCELULIAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.

-I- TISSUB SPECIFICITY: Expressed in mature B-cells, but not in T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells or monocytes.
-!- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia
(T-ALL) by a chromosomal translocation t(4;16) (q26;p13) which
                                      g C.H.; a TNF homologue implicated in B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIN; 109545; -.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:000866; C:plasma membrane; TAS.

GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0004872; F:receptor activity; TAS.

GO; GO:0007165; P:signal translocation; TAS.

B GO; GO:0007165; P:signal translocation; TAS.

M Dolymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.

M Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembrane.

T DOWAIN 1 54 Extracellular (Potential).

T TRANSMEM 55 77 Signal-anchor for type III membrane

T TRANSMEM 55 77 Signal-anchor; Transmembrane.

T TRANSMEM 77 184 Cytoplasmic (Potential).

T TRANSMEM 78 184 Cytoplasmic (Potential).

T TRANSMEM 77 41 TURE-Cys.
                                                                                                                                                                                                                                           MEDLINE=21170294; PubMed-10973284; V. G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.; Hakil and Tall-I and receptors BCWA and TACI: system for regulating humoral immunity.";
       Littau A., Grossman A., Haugen H., Foley K., Blumberg H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL2/TNFRSF17 oncogene
                                                                                                                                                                                                                           FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF.
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By similarity.
By similarity.
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Genew; HGNC:11913; TNFRSF17.
MIM; 109545; --
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Moore M., Littau A., Grossman A.,
Harrison K., Kindsvogel W., Clegg
"TACI and BCWA are receptors for a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nat. Immunol. 1:252-256(2000).
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                                                                                                                                                      Nature 404:995-999(2000).
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PIR; S43486; S43486
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058291; AAH58291.1; -.
GO; GO:0004872; F:receptor activity; IEA.
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AAH58291;
                                                                   Receptor.
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Klauener R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jozdan H., Moore T., Max S.I., Wang J., Hasieh F.,
Stapleron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toohlyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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277AF11E2767D932 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor receptor superfamily, member 17.
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                                                                                                                                                                                                                                      Score 964; DB 1;
Pred. No. 1.4e-81;
0; Mismatches 0;
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MEDLINE=22388257; PubMed=12477932;
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Scares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor receptor superfamily, member 17.
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20139 MW; C7ACF9B40FC5531A CRC64;
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                99.6%; Score 960; DB 2; Le 99.5%; Pred. No. 3.3e-81;
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                                                                                        Best_Local Similarity 99.5%;
Matches 183; Conservative
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   184 AA;
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                                                                                 1 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCL
                                    Gaps
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MEDLINE=990601155; PubMed=9846698;
Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
"The characterization of murine BCMA gene defines it as a new member of the tumor necrosis factor receptor superfamily.";
Int. Immunol. 10:1693-1702(1998).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
                                 0; Indels
     99.5%; Pred. No. 3.3e-81;
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                            1; Mismatches
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Name=Tnfrsf17; Synonyms=BCMA, BCM;
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                              Matches 183; Conservative
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Best Local Similarity
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088472;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the burspean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
transcriptome based on functional annotation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Receptor for TNPSF13B/BLyS/BAFF and TNFSF13/APRIL.
-Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and UNK (By similarity).
-!- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
-!- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
-!- ALTERNATIVE PRODUCTS:
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Alternative splicing; Immune response; Receptor; Signal-anchor;
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Signal-anchor for type III
protein (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytoplasmic (Potential)
TNFR-Cys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isold=088472-2; Sequence=VSP 006507; TISSUE SPECIFICITY: Detected in spleen, thymus heart, and at lower levels in kidney and lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59.3%; Score 572; DB 1; 62.6%; Pred. No. 4.3e-45; cive 21; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=088472-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VSP
                                                                               (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF061505; AAC23799.1; -.
EMBL; AK020247; BAB32038.1; -.
EMBL; BC027519; AAH27519.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20442 MW;
                 60,770 full-length cDNAs."
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
36
32
36
91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49
                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 117; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
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Gaps

8;

41; Indels

Conservative

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LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                                                                                         120 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
    63
                          SEQUENCE FROM N.A. (ISOFORM 1).

STRAIN=CS7BL/6J; TISSUE=Small intestine;

CKAZAKI Y., Furuno N., Saitor A., Adachi J., Bono H., Kondo S.,

Nikaido I., Osato N., Saitor R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nikaido I., Osato N., Saitor R., Suzuki H., Yamanaka I., Kiyosawa H.,

Nagir K., Tomaru Y., Hasegawa Y., Nogami A., Schombach C., Gojobori T.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,

Balake J.A., Saitolodid M., Gissi C., Godzik A., Gough J.,

Ranai A., Kawaji H., Kawasawa Y., Medaraski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,

Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,

Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwal K.,

Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1 Tumor necrosis factor receptor superfamily member 13C (B cellactivating factor receptor) (BAFF receptor) (BAFF receptor)
(B-cell maturation defect).

Name=Thfrsfl3C; Synonyms=Baffr, Bcmd, Br3;
MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21475520; PubMed=11591325;
Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
Canacro M.P., Grewal I.S., Dixit V.M.;
"Identification of a novel receptor for B lymphocyte stimulator that
is mutated in a mouse strain with severe B cell deficiency.";
Curr. Biol. 11:1547-1552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "BAFF-R, a newly identified TNF receptor that specifically interacts with BAFF.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BALB/C; TISSUE=B-Cell lymphoma; MEDLINE=21442025; Pubmed=11509692; DOI=10.1126/science.1061965; Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L., Ambrose C.;
                                                                                                                                                                                                                                                                                                                                                                                                       175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 293:2108-2111(2001).
                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                             EKPTHTR 185
                                                                                                                                                                                                                                                        EKSISAR 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                 64
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., William D.G., Wynshaw Boris A., Yanaglaswa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayateu N., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa I., Yasunishi A., Yoshino M., Waterston R., Lander B.S., Rogers J., Blincy E., Hayashizaki Y.;

Blincy E., Hayashizaki Y.;

"Analysis of the mouse transcriptome based on functional annotation of Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 OCSQNEYFDSLLHACIPCOL-----GINAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE SPECIFICITY: Highly expressed in spleen and testis;
TISSUE SPECIFICITY: Highly expressed in spleen and testis;
detected at lower levels in lung and thymus.
DISBASE: Defects in Thriffiz are a cause of severe B-cell
deficiency. B-cell deficient strain A/WySnJ has a 4.7 kb inserti.
in the BAFFR gene leading to an altered C-terminus. The mutant R is not detectable. B-cell lymphopoiesis is normal, but the life span of peripheral B-cells is much reduced.
SIMILARITY: Contains 1 TNRR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promotes the survival of mature B-cells and the B-cell response. -!- SUBCELLULAR LOCATION: Type III membrane protein (Probable). -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                       MEDILINE-21614654; PubMed=11747827; Hau B.L., Clise-Dwyer K., Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K., Hilbert D.M., Hayes C.E., Cancro M.P.; "Competition for BLyS-mediated signaling through Bcmd/BR3 regulates
                                                                                                                                                                                                                                                                                                                                                                                          peripheral B lymphocyte numbers.";
Curr. Biol. 11:1986-1989(2001).
-!- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLyS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal-anchor for type III membrane protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys (incomplete).
By similarity.
By similarity.
N-linked (GlCNAC. . .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AR373847; AAK91827.1; -.
EMBL; AK008142; BAB25490.1; -.
HSSP; O96R3; 1.0QE.
MGD; MGI:1919299; Thfraff13c.
Alternative splicing; Glycoprotein; Immune response; Receptor; Signal-anchor; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 AA; 18798 MW; 28BC7C1A02FB87EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (in isoform 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12.1%; Score 116.5; ilarity 29.4%; Pred. No. 0.01 Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId=Q9D8D0-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (or send an email to license@isb-sib.ch)
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/FTId=VSP_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal-anchor;
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simil
Matches 50; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=2;
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DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                            PUNCTION
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80

21 ÓCNÓTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALÓPQEGSALRPDVALLVGAPALL

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DOMAIN
TRANSMEM
DOMAIN
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셤
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                                   81 GLILALTLVGLVSLVSWRWRQQLRTASPDTSEGVQQE-----SLENVFVPSSET-- 129
  57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OCNOTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALOPOEGSALRPDVALLVGAPALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor (FASL (Apo-1 antigen)
                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
1TRAF3 binding protein.
Name=Tnfsf13c;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musinae; Musinae; Musinae; Musinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                            112 BIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 175;
                                                                                                               112 EIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Liston N.A. Sato T.-A.;
Mizuno K., Irie S., Sato T.-A.;
Mizuno K., Irie S., Sato T.-A.;
Submitted (FRB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF350577; AAL83314.1; -.
HSSP; Q96RJ3; 10QE.
MGD; MGI:1919299; Infref13c.
SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 6 preceptor) (Apoptosis-mediating surface antigen FAS) (CD95 antigen).
                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 116.5; DE
Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 th 12.1%;
Similarity 29.4%;
50; Conservative 2:
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                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WCBI_TaxID=10090;
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NCBI_TaxID=9913;
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P51867;
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OBR4

OBR4

OC 08R4

OC 01-7

OC 01-7

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OC MAMM

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or.send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KDEFKNTGSG-----LLGMANIDL------EKSRTGD--EIILPRGLEYTVEECTCED 130
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                       (aspartate-specific cysteine proceases) mediating apoptosis. FAS-
mediated apoptosis may have a role in the induction of peripheral
tolerance, in the antigen-stimulated suicide of mature T-cells, or
both (By similarity).
-!- SUBGNIT: Binds DAXX and RIPK1 (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- DOMAIN: Contains a death domain involved in the binding of FADD,
and maybe to other cytosolic adaptor proteins.
-!- SIMILARITY: Contains 1 Take Contains 3 TNFR-Cys repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNAC. . .) (Potential).
N-linked (GlCNAC. . .) (Potential).
activation which initiates the subsequent cascade of caspases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS00652; TNFR NGFR 1; 2.
PROSITE; PS50050; TNFR NGFR 2; 2.
Apoptosis; Glycoprotein; Receptor; Repeat; Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4D88A90E9E1F4892 CRC64;
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22.1%; Pred. No. 2.3;
iive 33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNFR-Cys 2.
TNFR-Cys 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000488; Death.
InterPro; IPR011029; DEATH like.
InterPro; IPR008063; Fas receptor.
InterPro; IPR001368; TNFR c6.
Pfam; PF00531; Death, 1.
Pf00020; TNFR c6; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36445 MW;
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SMART; SM00005; DEATH; 1.
SMART; SM00208; TNFR; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U34794; AAC48546.1; -. HSSP; P25445; 1DDF.
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ses 51; Conserv
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Transmembrane

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Signal-anchor;
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                                                  TRANSMEM
                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                            Query Match
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                           DOMAIN
                                                                                                DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note-No experimental confirmation available;
TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
in resting B-cells. Detected at lower levels in activated B-cells,
resting CD4+ T-cells, in thymus and peripheral blood leukocytes.
SIMILARITY: Contains I TNPR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M., Cancro M.P., Grewal I.S., Dixit V.M.;

Cancro M.P., Grewal I.S., Dixit V.M.;

"Identification of a novel receptor teo B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";

Curr. Biol. 11:1547-1552(2001).

-!- PUNCTION: B-cell receptor specific for TNFSF13B/TALLI/BAFF/BLyS.

Promotes the survival of mature B-cells and the B-cell response.
-: SUBCELLULAR LOCATION: Type III membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "BAPP-R, a newly identified TNF receptor that specifically interacts with BAFP.",
                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
1-OCT-2004 (Rel. 45, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor
                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21442025; PubMed=11509692; DOI=10.1126/science.1061965; Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L., Cachero T.G., Hession C., Schneider P., Sizing I.D., Millen C., Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L., Ambrose C.;
                           173
                                                                       254 IMH-----DNVH----ETAEQKVQLLRNWYQSHGKKNAYCTLTKSLPKALA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001368; TNFR C6.
PROSITE; PS00652; TNFR NGFR 1; FALSE NEG.
PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
3D-etructure; Alternative splicing; Immune response; Receptor;
                           CIKSKPKVDSDHCFPLPAMEEGATILVT----TKTNDYC---KSLPAALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=2;
IsoId=Q96RJ3-2; Sequence=VSP_006505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=Q96RJ3-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 10QE; X-ray; K/L/M/N/O/P/Q/R=16-46.
PDB; 10SX; NWR; A=1-61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
TISSUE=B-cell lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                            Name=TNFRSF13C; Synonyms=BAFFR, BR3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21475520; PubMed=11591325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF373846; AAK91826.1; -.
                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 293:2108-2111(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS
                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                HUMAN
                           131
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                                                                                                                                                                                                                     096RJ3;
                                                                                                                                                                         T13C_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 RIGDEIILPRGLEYTVEECTC-----EDCIKSKPKVDSDHCFPLPAMEEGATILVTTK 160
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PubMed=14973122;
Piel J., Hofer I., Hui D.;
"Evidence for a symbiosis island involved in horizontal acquisition of pederin biosynthetic capabilities by the bacterial symbiont of
                                                                                                                                                                                                                                                                                                                                                                           8 CSQNEYFDSLLHACIPCQL-----RCSSNTP--PLTCQRYCNASVTNSVKGTNAIL
                                                                                                                                                                                                                                                                                                                                                                                                                       CVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALQPQESVGAGAGAALPLPGLL
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                            membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A polyketide synthase-peptide synthetase gene cluster from an uncillured bacterial symbiont of Paederus beetles."; Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 9.6%; Score 92.5; DB 2; Length 334; Local Similarity 25.0%; Pred. No. 3.4; Conservative 22; Mismatches 65; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 184;
Extracellular (Potential).
Signal-anchor for type III me
protein (Potential).
Cytoplasmic (Potential).
TWFR-Cys (incomplete).
By similarity.
By similarity.
                                                                                                                                                                                                                                                                                                                          65; Indels
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                                                                                                                                                                                                                         F2BFB98099A27138 CRC64;
                                                                                                                                                                        P -> PA (in isoform 2). /FTId=VSP_006505.
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Last annotation update)
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J. Bacteriol. 186:1280-1286 (2004).
EMBL; AY326023, AA547559.1;
GO; GO:0008415; F:acyltransferase activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
InterPro; IPR001227; Ac transferase.
Fam; PF00699; Acyl transferase.
Acyltransferase; Transferase.
SEQUENCE 334 AA; 38018 MW; 6C42D1FFEC5E35F3 CRC
                                                                                                                                                                                                                                                                       9.6%; Score 93; DB 1
86.5%; Pred. No. 1.6;
ve 20; Mismatches
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                                                                                                                                                                                                                            184 AA; 18863 MW;
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Matches 48; Conservative 2
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Name=pedC;
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35
32
35
143
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STRAIN=Stock d4-2;
Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
Cohen J., Meyer E., Sperling L.;
"High coding density on the largest Paramecium tetraurelia somatic
                                                                                                                                                                               chromosome.";
Curr. Biol. 0:0-0(2004)
       [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-Stock d4-2;
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                                                                      70 VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCE 129
                                                                                                                        121 THVENILFNLİKQARLFDEYCNAGAMLLVIDHİD---------TFSTTPAFSK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FDRLIH------THPALFMVQYALAKSLLARGLPAPDFLIGASLGEFIAISLAGD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Piel J., Hofer I., Hui D., "Evidence for a symbiosis island involved in horizontal acquisition of pederin biosynthetic capabilities by the bacterial symbiont of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 FDSLLHACIPCOLRCSSNTPPLTCQRYCNAS -- VTNSVKGTNAILWTCLGLSLIISLA--
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01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative surface protein with EGF domains and furin-like repeats.
ORFNames=PTWB.409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A polyketide synthase-peptide synthetase gene cluster from an uncultured bacterial symbiont of Paederus beetles.";
Proc. Natl. Acad. Sci. U.S.A. 99:14002-14007(2002).
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                                                                                                                                                                                                           DCIKSKPKVDSDHCFPLPAMEEGATILVT----TKTNDYCKSLPAALS 173
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EMBL. AY28023; AAS4759-1, -.
ACYLtransferase; Transferase.
SEQUENCE 334 AA; 38018 MW; 6C42D1FFEC5E35F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                      334 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 3005 AA.
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MEDLINE=22294974; PubMed=12381784;
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(TrEMBLrel. 27, I
(TrEMBLrel. 27, I
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Best Local Similarity
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NCBI_TaxID=176282;
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PubMed=14973122;
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FDRLIH-
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03-MAR-2004
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-----CLCKDGFYETIEKMCQPCDMTCKTCVSQSTKCLT 1313
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MEDINE-2135935; PubMed=1466286;

DOI=10.1128/JB.183.16.4823-4838.201;

Mobiling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

A Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L.A., Soucaille P.,

Daly M.J., Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
if Genome sequence and comparative analysis of the solvent-producing
if J. Bacterium accetobutylicum.";

"Genome sequence and comparative analysis of the solvent-producing
if J. Bacteriul (193:4823-4838 (2001).

-: FUNCTION: Part of a binding-protein-dependent transport system.

Probably responsible for the translocation of the substrate across

the membrane (By similarity).

-: SUMILARITY: Belongs to the binding-protein-dependent transport
                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                       1231 KCICDSGYYFNTS-TKQCEACNITCKECQSVS--------QCIECEPMTRYNDR 1275
                                                                                                                                                                                                                                                                                                                                                                                   87 DEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVE-----ECTCEDCIKSKPKV-- 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 -----DSDHCFPLPAMEE--GATILVTTKTNDYCKSLPA----ALSATEIEK 179
                                                                                                                                                                                                                                                                                             ------NASVINSVKGINAILWTCLGLSLIISLAVFVLMFLLRKISSEPL----K
                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clostridium acetobutylicum.
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                           Indels 104;
                                                                                                                 Length 3005;
Nowak J.K., Migdaiski A., Gromadka R., Zagulski M.;
Submitred (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR648612; CAH03606 1;
SEQUENCE 3005 AA; 343821 MW; D8CC6A247876A5A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
permease component.
                                                                                                                                                           59;
                                                                                                                 9.2%; Score 89; DB 2; 20.3%; Pred. No. 71;
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EMBL, AE007858; AAK81542.1; -
PIR, C97344; C97344; C97346; C97360; C:membrane; IEA.

GO, GO:0016020; C:membrane; IEA.
                                                                                                                                                             26; Mismatches
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                                                                                                                                                           48; Conservative
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Best Local Similarity
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Paramecium tetraurelia. Eukaryota, Alveolata, Ciliophora, Oligohymenophorea, Peniculida,

Paramecium. NCBI_TaxID=5888;

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Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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STRAIN=BALB/c; TISSUE=Testis;
Fargeas C.A., Huttner W.B., Corbeil D.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY099088; AAM2845.1; -.
MGD; MGI:1100886; Proml.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD, MGI:1100886; Proml.
GO: 000:009303; c:brush border; IDA.
GO: GO:0005897; C:integral to plasma
GO; GO:0005902; C:micgovillus; IDA.
                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                               01-JUN-2003 (TEEMBLrel. 24, 01-MAR-2004 (TEEMBLrel. 26, Prominin-1 T3 isoform.
                              :||:: ::|:
267 LQDAATQLNTNLSS 280
  173 ---SATEIEKSISA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 ---SATEIEKSISA 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prominin T4 isoform.
Name=Prom1; Synonyms=Prom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF05478; Prominin; SEQUENCE 809 AA; 90609
                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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01-JUN-2003
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                                                                                                                       RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 ALGLIYGQIMKRIILPQAIRVVIPPCGNEFIAMIKDTSLVSVITMEELLRKAQLLVSSSG 183
                                                                                                                                                                                                                                                                                                                                                                                                                63 SLIISLAVFV--LMFLLRKISSEPLKDEF----KNTGS------GLLGMANIDLEKSR 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
                                                                                                                                                                                                                                                                                                                                                                   63
                                                                                                                                                                                                                                                                                                                     16 SLIHACIPCQLRCSSNTPPLTCQRYCNASV-----TNSVKGTNAI----LWTCLGL
                                                                                                                                                                                                                                                                                                                                                                SSLNKVI PVLLDGTRITLLLTCSSIIIGCIIGTIIAMFKTSSVKVLNLIGKFYTWILRGT
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                               Query Match 9.2%; Score 88.5; DB 2; Length 217; Best Local Similarity 24.8%; Pred. No. 5; Matches 55; Conservative 25; Mismatches 77; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BALB/C; TISSUE=Testis;
Regeas C.A., Huttner W.B., Corbeil D.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
BMBL; A7223521; AA072429-1; -.
MGD; MGI:1100086; Proml.
GO; GO:0005903; C:brush border; IDA.
GO; GO:0005903; C:integral to plasma membrane; IDA.
GO; GO:0005902; C:integral to plasma membrane; IDA.
GO; GO:0005902; C:integral to plasma membrane; IDA.
GO; GO:0005902; C:integral to plasma membrane; IDA.
FGM: PFROM: PROMP19; Prominin.
SEGUENCE 804 AA; 89983 MW; CFC9D6E8BCF9FF16 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184 DAVTPYLFAĞIFYLİLTİRİĞIFSK------İEKKLS 215
                    InterPro; IPR000515; BPD transp.
InterPro; IPR010055; HBORO ABC 3TM.
Pfam; PF00528; BPD transp 1; 1.
TIGRFAMs; TIGR01726; HEORO perm 3TM; 1.
PROSITE; PS50028; ABC TM1; 1.
COMPLETE PTCCOMP: TAIRNED TRANSPORT.
SEQUENCE 217 AA; 23743 MW; 36738BCDC0DE8A2F CRC64;
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Last annotation update)
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22.7%; Pred. No. 30;
tive 30; Mismatches
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GO:0006810; P:transport; IEA.
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QBOXB3
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168 GFVANQQTRTRIKGTQK-----LAKSNPRDFQTLLTETPKQIDYVVEQYTNTKNKA 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53; Gaps
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=BALB/c, TISSUE=Testis;
Fargeas C.A., Hutcher W.B., Corbeil D.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY223522; AAO72430.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inin; 1.
90605 MW; BC991E100C623AE1 CRC64;
                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane; IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.0%; Score 86.5; DB Best Local Similarity 22.7%; Pred. No. 31; Matches 44; Conservative 30; Mismatches
809 AA
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[5]
SEQUENCE
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Q8BH12
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                                                                                                                                                                    117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
                                                                                                                                                                                                          78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-BIIL---PRGLEYTVEECTCE--- 129
                                                                                                                                                                                                                                                                130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
                                                                                                                                                                                                                                                                                219 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMS$SLKS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAINE-CSTBL/6J; TISSUE=Testis;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cons.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                     18 LHACIPCOLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4931440N24 product:prominin, full insert sequence.
Name=Prom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                           53;
                                                                                             9.0%; Score 86.5; DB 2; Length 823; 22.7%; Pred. No. 31; ive 30; Mismatches 67; Indels 53
                                                     Pfam; PF05478; Prominin; 1.
SEQUENCE 823 AA; 92225 MW; 9EF01A18DB84EFAC CRC64;
            GO; GO:0005887; C:integral to plasma membrane; IDA. GO; GO:0005902; C:microvillus; IDA. InterPro; IPR008795; Prominin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA cloning.";
 GO:0005903; C:brush border; IDA.
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MEDLINE=99279253; PubMed=10349636;
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STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-21085660; PubMed=11217851;
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"High-efficiency full-length C:
Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                                                                                                                                                                     ---SATEIEKSISA 183
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272 LQDAATQLNTNLSS 285
                                                                                                                         44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                            Best Local Similarity
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Carrain-Carrain A. Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashlaume W., Burda S., Ehruno M., Hanagaki T., Hara A., Hashlaume W., Hayashida K., Hayatsu W., Hiraoka T., Harozan T., Hayashida K., Hayatsu W., Hiraoka T., Hirozane T., Ach H., Kawai J., Kojima Y., Konno H., Konno H., Konno H., Konno H., Konno H., Konno H., Konno H., Konno M., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nahi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saito R., Saito R., Saito R., Saito R., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Sogabe Y., Tagami M., Hayashizaki Y., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y., Lakata A., Muramatsu M., Hayashizaki Y., Rubb, MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI., MGI
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01-007-2004 (TrEMBLrel. 28, Last annotation update)
Prominin T1 isoform (Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4932416E19 product:prominin, full
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                                 STRAIN-CS7EL/6J; TISSUE=Testis; MEDLINE=20530913; PubMed=11076861; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Sumino K., Marsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., REKEN integrated sequence analysis (RISA) system-384-format gequencing pipeline with 384 multicapillary sequencer.";
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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SEQUENCE 827 AA; 92714 MW; DBCASED2DF401A18 CRC64;
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22.7%; Pred. No. 31;
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01-WAR-2003 (TrEMBLrel. 23, Last seq
01-OCT-2004 (TrEMBLrel. 28, Last ann
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272 LQDAATQLNTNLSS 285
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FROM N.A.
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53; Gaps

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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

A trausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Zeeberg B. Buetow K.H.; Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B. Buetow K.H.; Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A patchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B connetein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Perers G.J., Abramson R.D., Mullahy S.J.,

B soak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rachey J., Helton B., Ketreman M., Madan A., Young A.C., Sheckbenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Sheckbenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Brakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                        117 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 167
                                                                                                                                                                                                                                 78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---- 129
                                                                                                                                                                                                                                                                                                                     ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
                                                                                                                                                                                                                                                                                                                                                          219 FSDLDGIGSVLGGRIKDQLKPKV------TPVLEBIKAMATAIKQTKDALQNMSSSLKS 271
                                                                                                                                              18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                                                                                                                                                                                                                                                          168 GFVANQQTRIRIKGTQK-----LAKSNFRDFQTLLTFTPKQIDYVVEQYINITKNKA
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                             DB 2; Length 834;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC028286; AAH28286.1; -.
  Pfam; PF05478; Prominin; 1.
SEQUENCE 834 AA; 93444 MW; SABA26C80F636E45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                    67;
                                                         Query Match 9.0%; Score 86.5; D
Best Local Similarity 22.7%; Pred. No. 32;
Matches 44; Conservative 30; Mismatches
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GO; GO:0005903; C:brush border; IDA.
GO; GO:0005887; C:integral to plasma
GO; GO:0005902; C:microvillus; IDA.
InterPro; IPR008795; Prominin.
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01-JUN-2002 (TrEMBLrel. 21, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last anno
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272 LQDAATQLNTNLSS 285
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Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W., Furuda S., Furuno M., Hangaki T., Haracka T., Hirozane T., Hayatsu N., Hirancto K., Hiracka T., Hirozane T., Hayatsu N., Hirance K., Hiracka T., Hirozane T., A Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kawai J., Kojima Y., Konno H., Konno H., Kowa T., Kurihara C., Marsuka M., Murata M., Roya S., Kurihara C., Marsuki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., A Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AR030215; AAO11840.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

C STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; Pubmed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Nakamura K., Nishine T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramansu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECUENCE FROM N.A.
SECUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itch M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Mornalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                          RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                           STRAIN=BALB/c; TISSUE-Testis;
Fargeas C.A., Huttner W.B., Corbeil D.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0005987; C:integral to plasma membrane; IDA
GO; GO:0005902; C:microvillus; IDA.
InterPro; IPR008795; Prominin.
                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Testis;
MEDLINE-21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Testis;
The PANTOM Consortium,
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                                     SEQUENCE FROM N.A
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WCBI_TaxID=10090;
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membrane; IDA

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Qeccil;
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                                           10;
                                                                            228 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEEIKAMATAIKQTKDALQNMSSSLKS 280
                                                                                                                     130 ----DCIKS------KPKVDSDHCFPLPAMEEGATILVTTK-TNDYCKSLPAAL-- 172
                                                              18 LHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVFVLMFLL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 RKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGD-EIIL---PRGLEYTVEECTCE---
                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                           53;
                                                                                                                                                                                                                                                                                                                         Prominin 1 precursor (Prominin-like protein 1) (Antigen AC133
                      DB 2; Length 842;
                                          67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                 W., Buck D.;
to the EMBL/GenBank/DDBJ databases
 842 AA; 94478 MW; 734C10D715E5BC92 CRC64;
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                     9.0%; Score 86.5; D 22.7%; Pred. No. 32; ative 30; Mismatches
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MGD; MGI:1100886; Proml.
GO; GO:0005903; C:brush border; IDA.
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281 LQDAATQLNTNLSS 294
                                          Conservative
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Submitted (DEC-1997)
                     Query Match
Best Local Similarity
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                                          44;
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SEQUENCE
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126 LVGCFFCMCRC-----CNK-CGGEMHQRQKQNAPCRRKCLGLSLLVICLLMSLGIIY 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 FSDLDGIGSVLGGRIKDQLKPKV-----TPVLEFIKAMATAIKOTKDALQNMSSSLKS 280
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Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Dipodascaceae, Yarrowia.
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GENOLEVURES;
Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
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N-linked (GlCNAC. .) (Pote
N-linked (GlCNAC. .) (Pote
S -> N (in Ref. 2).
K -> N (in Ref. 2).
Massing (in Ref. 2).
Massing (in Ref. 2).
G -> D (in Ref. 2).
G -> D (in Ref. 2).
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Cytoplasmic (Potential).
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01-0CT-2004 (TrEMBLrel. 28, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
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GO, GO:0005887; C:integral to plasma GO; GO:0005902; C:microvillus; IDA. InterPro; IPR008795; Prominin. Pfam; PFG478; Prominin; 1. Glycoprotein; Signal; Transmembrane.
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281 LQDAATQLNTNLSS 294
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TRANSMEM
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SMART; SM00261; FU; 6.
SMART; SM00219; TYTKC; 1.
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Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boistame A., Boyer J., Cattolico L., Confanioleri F., de Darnvar A., Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Karrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicolaki M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesclowski-Louvel M., Westhof E., Witth B., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Whincker P., Souciet J.L.;
                                                                                                                                                                                                                                                                                                                                                                                         813 CLETVVASIŚGTPTTVINNICTTSAPVDPCLETVTASVSGSTTIVTNDICKTVDPCITTE 872
                                                                                                                                                                                                                                                                                                                                                                                                                    70 VFVLMFLLRKISSEP---LKDEFKNTGSGLLGMANIDLE---KSRTGD-----E 112
                                                                                                                                                                                                                                                                                                                                                                                                                                   873 VVT-----VSGTPATWITKDVCQTIADPCLETAIVILSGTPAIVTKDICTSADPCVETE 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SDHCFPLPAMEEGAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                926 VVTVSGTESTV---TKNSCITSTPVADPCVVTETISSGTITEVITRDICTPAPTPVVTST 982
                                                                                                                                                                                                                                                                                                                                                                21 CIPCQLRCSSNTPPLTCQRYCNAS------VTNSVKGTNAILWT--CLGLSLIISLA 69
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Extensive gene duplication in the early evolution of animals before the parazoan-eumetazoan split demonstrated by G proteins and protein tyrosine kinases from sponge and hydra.";
J. Mol. Evol. 48:646-653(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=21601119; PubMed=11738833;
Suga H., Katch K., Mayata T.;
"Sponge homologs of vertebrate protein tyrosine kinases and frequent domain shufflings in the early evolution of animals before the parazoan-eumetazoan split.";
                                                                                                                                                                                                                                                                                                                                      70;
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MEDLINE-99246375; PubMed-10229568;
Suga H., Koyanagi M., Hoshiyama D., Ono K., Iwabe N., Kuma K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ephydatia fluviatilis.
Eukaryota, Metazoa, Porifera, Demospongiae, Ceractinomorpha,
Haplosclerida, Spongillidae, Ephydatia.
NCBI_TaxID=31330,
                                                                                                                                                                                                                                                                                                         8.9%; Score 86; DB 2; Length 1309;
14.0%; Pred. No. 56;
ve 17; Mismatches 78; Indels
                                                                                                                                                                                                                                                                    EMBL, CR382129; CAG81904.1; -.
SEQUENCE 1309 AA; 137079 MW; 7D2E2927115D6CC2 CRC64;
                                                                                                                                                                                                                                           Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 IILPRGLEYTVEECTCEDCIKSKPKVD------
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                                                                                                                                                                                                                                                                                                                                       52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein tyrosine kinase.
Name=EfPTK178;
                                                                                                                                                                                       Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                         Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                             STRAIN=CLIB99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57 WTCLGLSLIISLA---VFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Gaps
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicacaes; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Boweer L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Sakin M., Shinn P., Southwick A., Shinozaki K.,
Buvis R.W., Ecker J.R., Theologis A.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
GO:0016020; C:membrane; IEA.
GO:0005524; F:ATP binding; IEA.
GO:000506; F:epidermal growth factor receptor activity; IEA.
GO:0016740; F:transferae activity; IEA.
GO:0006468; P:protein amino acid phosphorylation; IEA.
GO:0007169; P:transmembrane receptor protein tyrosine kin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            821 LRP------EXLPPDATRLIITPETALEQGOVL 847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.9%; Score 85.5;
                                                                                                                                                                                               InterPro; IPR006211; Furin-like.
InterPro; IPR006211; Furin-like.
InterPro; IPR006211; Furin-like.
InterPro; IPR006213; Furin repeat.
InterPro; IPR001009; Kinase like.
InterPro; IPR001009; Kinase like.
InterPro; IPR001709; Prot Kinase.
InterPro; IPR001709; Prot Kinase.
InterPro; IPR001709; Prot Kinase.
InterPro; IPR001709; Fryr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase.
InterPro; IPR008266; Tyr_pkinase.
InterPro; IPR008269; Furin-like; I.
Pfam; PP001030; Recep_L domain; 2.
Pfam; PP001030; TYRKINASE.
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SEQUENCE FROM N.A.
STRAINE-GYBL/GA1 TISSUE-Oviduct;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Oviduct; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CONA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                               01-MRR-2003 (TrEMBLrel. 23, Created)
01-MRR-2003 (TrEMBLrel. 23, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last sequence update)
Mus musculus 2 days pregnant adult female oviduct cDNA, RIKEN full-
length enriched library, clone:E230011L17 product:protein tyrosine
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STRAIN=C57BL/6J; TISSUB=Oviduct;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Shibata M., Nishiro H., Itoh M., Itoh M., Nishiro H., Itoh M., Itoh M., Nishiro H., Itoh M., Vammura S., Hazama M., Nishino T., Harada A., Yamamoto R., Matsunato H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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STRAIN=CS7BL/6J; TISSUE=Oviduct;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Car
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
                                                                                                                                                                                                                                                                                                                                                                                                                           beta, full insert sequence. (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CS7BL/6J; TISSUB=Oviduct;
MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                        449 AA.
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STRAIN-C57BL/6J; TISSUE-Oviduct;
MEDLINE-21085660; PubMed=11217851;
1174 DGGATI 1179
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                                                                                                                                                                                                                                                                            Score 83.5; DB 2; Length 938;
Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Cholsne N., Robert C., Brottier P., Wincker P., Cattolico L.
Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Rudd
Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                              28; Indels
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Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AL096855, CAB51067.1; -.
BIR, 113009, T13009.
GO; GO:0007242; P:intracellular signaling cascade; IEA.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR001683; PX.
Pfam; PF00787; PX; 1.
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                                                                                                                                                                                                       11 protein.
938 AA; 103602 MW; 3E78395D65D75C95 CRC64;
                       GO; GO:0007242; P:intracellular signaling cascade; IEA.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR001683; PX.
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypotherical protein T24C20_80.
Name=T24C20_80,
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PROSITE; PS0190; CYTOCHKOME C; UNKNOWN 2.
PROSITE; PS50195; PX; 1.
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PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_2.
PROSITE; PS50195; PX; 1.
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     EMBL; AY091078; AAM13898.1;
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SEOUENCE 1998 AA;
                                                                                               Pfam; PF00787; PX; 1.
SMART; SM00312; PX; 1
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ses 37; Conserv
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DGGATI
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                                                                                                                                                                                                                              SEQUENCE
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Nature 420:563-573 (2002).
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Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saitoh H., Sakai K., Sakai K., Sakazuka N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogbe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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STRAIN=C57BL/6J; TISSUE=Thymus;
The FANTOM COnsortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched
library, clone:A63004301 product:protein tyrosine kinase 2 beta, fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 KSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEAENMADLIDGYCR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.6%; Score 83; DB 2; Length 449; 26.9%; Pred. No. 35; Live 13; Mismatches 34; Indels
                                                                                                                                                                                                                                                         MGD; MGI:104908; Ptk2b.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004672; F:protein kinase activity; IDA.
GO; GO:000468; P:protein amino acid phosphorylation; IDA.
InterPro; IPR009065; FERM.
InterPro; IPR011009; Kinase_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D3565BCBA7D32B84 CRC64;
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MEDLINE-99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE-21085660; PubMed=11217851;
RIKEN FANTOM CONSOTTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51577 MW;
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PROSITE; PS50057; FERM_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 AA;
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88 BPKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
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STRAIN=C57BL/6J; TISSUE=Thymus; MEDLINE=20499314; PUNGd=11042159; MEDLINE=20499314; PUNGd=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Noxmalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Harando K., Hiraoka T., Hirozane T., Hori B., Indian K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Itoh M., Kodawa I., Kouda M., Koya S., Kurihara C., Mareuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sakai C., Sakai K., Sakazume N., Sano H., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                              MEDLINE-20530913; PubMed=11076861; MEDLINE-20530913; PubMed=11076861; MEDLINE-20530913; PubMed=11076861; MEDLINE-20530913; PubMed=11076861; Malana K., Naganai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matemuro H., Sakaguchi S., Ikegami T., Kashiwagi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Rishika Saquence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.6%; Score 83; DB 2; Length 474; 6.9%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:104908; Ptk2b.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0004672; F:protein kinase activity; IDA.
GO; GO:0004672; F:protein amino acid phosphorylation; IDA.
InterPro; IPR000299; Band 4.1.
InterPro; IPR009065; FERM.
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DHHC zinc finger domain, putative.
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PROSITE; PS50057; FERM_3; 1.
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Local Similarity
les 54; Conserv
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                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9940;
                                                                                                  STRAIN=CLIB99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fas protein.
Name=Fas;
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Matches
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SORERCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 NKWKKINLFIF-CQGIVKILIFHFFLLMFLINYILSIVTPPGFIFNTEEWVFKDFGEN-- 63
                                                                                                             Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L., Shallom S.J., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Chackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Plorens L., Yates F.N. III, Raine J.D., Sinden R.E., Harris M.A., Cunningham D.A., Perser P.R., Bergman L.W., Vaidya A.B., van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J., Carucci D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S., Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E., Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V., Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C., Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A., Bespons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A., Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R., Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H., Nicaleki M., Oztas S., Ozier Kalogeropoulos O., Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A., Swennene D., Tekaia F., Wesolowski-Louvel M., Westhof E., Witth B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORFNames=YALIOCO83499;
Yarrowia lipolytica (Candida lipolytica).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Yarrowia.
                                                                                                                                                                                                                                                                              parasite Plasmodium yoelii yoelii.";
Nature 419:512-519(2002).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 GMANID---LEKSRIGDEIILPRGLEYTVEECTCEDCIKSKPKVDSDHC 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 NSNNIDDYLLEKKKTG------ERRFCKWCCKYKPD-RAHHC 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 8.6%; Score 82.5; DB 2; Length 164; Local Similarity 31.2%; Pred. No. 14; length 164; Nes 34; Conservative 12; Mismatches 34; Indels 28
            Plasmodium yoelii yoelii.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD003041; Znf DHHC; 1.
PROSITE; PS50216; ZF DHHC; 1.
SEQUENCE 164 AA; 19593 MW; CFDDF8E66B690FF1 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                   preliminary data.

EMBL, AABLO1002253; EAA18841.1; -.

EO, GO:046872; F:metal ion binding; IEA.

InterPro; IPR001594; Znf DHHC.

Pfam; PF01529; zf-DHHC; I.
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                                     NCBI_TaxID=73239;
                                                                     SEQUENCE FROM N.A
                                                                                                  PubMed=12368865;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29 SSNTPPLTCQRYCNASVTNSVKGTNAILWT--CLGLSLIISLA-VFVLMFLLRKISSEPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lymphocyte;
Takaqi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB011671; EAA37093.1; -.
Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A., Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J., Wincker P., Souciet J.L., "Genome evolution in yeasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 KDEFKNTGSGLLGMANIDLEKSRTGD-----EIILPRGLEYTV--BEC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88;
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.6%; Score 82.5; DB 2; Length 1142; Best Local Similarity 25.6%; Pred. No. 1e+02; Matches 46; Conservative 23; Mismatches 72; Indels 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5%; Score 82; DB 2; Length 327; ilarity 23.0%; Pred. No. 31; Conservative 25; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R InterPro; IPRO0488; Death.
R InterPro; IPRO0488; Death.
R InterPro; IPRO1029; DEATH_like.
R InterPro; IPRO10369; Tas receptor.
R InterPro; IPRO00369; Tas receptor.
R Pfam; PF00031; Death, 1.
R Pfam; PF00030; TARR c6; 3.
R PRINTS; PR01680; FASTRCEPTOR.
R SWART; SW00006; DEATH; 1.
R SWART; SW00008; TNRR; 3.
R PROSITE; PS06017; DEATH DOMAIN; 1.
R PROSITE; PS06052; TNRR NGFR 1; UNKNOWN_1.
R PROSITE; PS06052; TNRR NGFR 1; UNKNOWN_1.
R PROSITE; PS06050; TNRR NGFR 2; 2.
R SEQUENCE 327 AA; 36928 MW; 5CFEE844B2BE387A CRC64;
                                                                                                                                                                                                                                                              Genoscope;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR382129; CAG81898.1; -.
SEQUENCE 1142 AA; 121017 WW; 11D636A6296F1912 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0016020; C:membrane; IEA.
GO; GO:0004888; F:transmembrane receptor activity; IEA.
GO; GO:0006915; P:atmanne response; IEA.
GO; GO:0006955; P:ammune response; IEA.
GO; GO:0007165; P:signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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STANDARD;
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Q9QVP9;
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                                                                       ---ISSEPLKDEFKNTGSGLLGMANIDLEKSRTG------DEIILPRGLEYTVEEC 126
                                                                                                                       203 NGNCVSAASSDEGRQ----EMLTDVDLGKYIPSIAELMKITEVKEFVRRGM----EEA 253
                                 CSEGNEYTDKSHHSDKCIRCSVCDEEHGLEVEHNCTRTQNTKCRCKCKSNFFCNSSPCEHCN 143
                                                         PPLICO----RYCNASVTNSVKG----TNAILWTCLGLSLIISLAVFVLMFLLRK---- 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NOD; TISSUB=Thymus;
MEDLINB=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Mramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                         127 TCEDCIKSKPKVDSDHCPPLPAMEEGATIL----VTTKTNDYC---KSLPAALS 173
                                                                                                                                                                         254 KIDDIMH-----DNLH----ETARQKVQLLRKWYQSHGKKNAYCTLTKNLPKALA 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20530913; PubMed=11076861;
Shibate K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itch M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
                                                                                                                                                                                                                                                                                                       Mus musculus 2 days neonate thymus thymic cells cDNA, RIKEN full-
length enriched library, clone:E430023005 product:protein tyrosine
kinase 2 beta, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=NOD; TISSUE=Thymus;
MEDLINE=99279253; PubMed=10349636;
Carninci Hayaehizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-NOD; TISSUE-Thymus;
MEDLINE-21085660; PubMed=11217851;
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                                                                                                                                                                                                                                                                                (TrEMBLrel. 23,
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 409:685-690(2001).
                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                               Name=Ptk2b
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=NOD; TISSUBE-Thymus;

A Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,

A Adachi J., Barawa K., Akimura T., Hara A., Hashizume W.,

A Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

A Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,

A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Roya S.,

A Kuthara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

A Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

A Saaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,

A Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;

Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.

R HSSP: JAKOB 696; BAC40510.1; -.
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05-JUL-2004 (Rel. 44, Last annotation update)
Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
adhesion focal tyrosine kinase).
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       Kawai J.,
                                                                                                                                                                                                                                                                                                  Carninci P.,
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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0109; TYRKINASB.
SMART; SM00219; TYRCK kinase; 1.
SMART; SM00219; TYRC; 1.
SWART; SM00219; TYRC; 1.
PROSITE; PS50057; FRENM 3; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00101; PROTEIN KINASE TYR; UKXOWN 1.
PROSITE; PS00109; PROTEIN KINASE TYR; UKXOWN 1.
ATP-binding; Kinase; TYR; UKXOWN 1.
STAP-binding; Kinase; TYR; UKXOWN 1.
SROUENCE 967 AA; 111311 MM; D65ABC83847BA62F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005515; F:procein binding; IPI.
GO; GO:0004672; F:procein kinase activity; IDA.
GO; GO:0006468; P:protein amino acid phosphorylation; IDA.
InterPro; IPR000299; BERM.
InterPro; IPR009065; FERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1009 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Ptk2b; Synonyms=FAK2, PYK2, Raftk;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%; Score 82;
6.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR005189; Focal AT.
InterPro; IPR011009; Kinase like.
InterPro; IPR00719; Prot Kinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR008266; Tyr pkinase.
Pfam; PF03623; Pocal AT; I.
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Best Local Similarity 26.9%
Matches 29, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION SITE TYR-402, AND INTERACTION WITH NEDHROCYSTIN.

MEDLINE-21396557; PubMed=11493697; DOI=10.1073/pnas.171269898;

MEDLINE-21396557; PubMed=11493697; DOI=10.1073/pnas.171269898;

The Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;

"Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers phosphorylation of Pyk2.";

Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).

"I FONCTION: Involved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between meuropeptide activated receptors or neurotransmitters that increase calcium flux and the calcium flux and the regulate neuronal activity. Interacts with the Standard protein KV1.2. Its activation is highly correlated with the Stimulation of c-Jun N-terminal kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S., Pagztor L.M., White R.A., Groopman J.E., Avraham H.; "Identification and characterization of a novel related adhesion focal tyrosine kinase (RAFTK) from megakaryocytes and brain."; J. Biol. Chem. 270:27742-27751(1995).
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21113779; PubMed=11420674; DOI=10.1018/sj/onc/1204359;
Nakamura K., Yano H., Schaefer E., Sabe H.;
"Different modes and qualities of tyrosine phosphorylation of Fak and Pyk2 during epithelial-mesenchymal transdifferentiation and cell migration: analysis of specific phosphorylation events using site-directed antibodies.";
Oncogene 20:2626-2635(2001).
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                     PTPNS1 BINDING.
MEDLINE=99401000; PubMed=10469599;
Timms J.F., Swanson K.D., Marie-Cardine A., Raab M., Rudd C.E.,
Schraven B., Neel B.G.;
"SHPS-1 is a scaffeld for assembling distinct adhesion-regulated
multi-protein complexes in macrophages.";
Curr. Biol. 9:927-930(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               activity (By similarity). CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                         PHOSPHORYLATION SITES TYR-402; TYR-580 AND TYR-881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005189; Focal AT.
InterPro; IPR011009; Kinase like.
InterPro; IPR000119; Prot kinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR008266; Tyr pkinase.
InterPro; IPR008266; Tyr pkinase AS.
Pfam; PF000659; Pkinase 1.
                                                                                       MEDLINE=96070905; PubMed=7499242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000299; Band 4.1.
InterPro; IPR009065; FERM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:104908; Ptk2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; Q05397; 1K04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IntAct; 090VP9; -.
                                                       SEQUENCE FROM N.A.
                                                                         TISSUE=Brain;
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DR PRINTS; E.C.

DR PROBOR; PD000001; L.

DR SMART; SM00219; TyrKc; 1.

DR PROSITE; PS00660; FERM 1; FALSE NEG.

DR PROSITE; PS00101; PERM 2; FEALSE_NEG.

DR PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE_DOM; 1.

DR PROSITE; PS00101; PROTEIN KINASE_TRY; 1.

KW ATP-binding; Phosphorylation; Transferase; Tyrosine-protein kinase.

FT DOWAIN 425 683 Protein kinase.

FT DOWAIN 431 439 ATP (By similarity).

FT BINDING 457 ATP (By similarity).

FT DOWAIN 701 767 Pro-rich.

FT DOWAIN 868 1009 Procal adhesion targeting (FAT).

FT DOMAIN 868 1009 Pro-rich.

FT DOMAIN 868 1009 Pro-rich.

MOD_RES 402 402 Phosphoryrosine (by autocatalysis) (By similarity).

Phosphoryrosine (by autocatalysis) (By similarity).

Phosphoryrosine (by autocatalysis) (By similarity).

Phosphoryrosine (by autocatalysis) (By similarity).

Phosphoryrosine (by autocatalysis) (By similarity).
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TISSUB-Liver epithelium;
MEDLINE=97094711; PubMed=8939945;
Yu H., Li X., Marchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L., Wilm M., Andersegg R.J., Graves I.M., Earp H.S.,
"Activation of a novel calcium-dependent protein-tyrosine kinase. Correlation with c-Jun N-terminal kinase but not mitogen-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P7060; 088489; Q63201;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Sprague-Dawley; TISSUE-Brain; MEDLINE-95403356; PubMed=7673154; Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.; "Cloning and characterization of cell adhesion kinase beta, a novel protein-tyrosine kinase of the focal adhesion kinase subfamily."; J. Biol. Chem. 270:21206-21219(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            139 DSDHCFPLPAME-----EGATILVTTKTND------YCK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 RSIRCLPLEETQAVLQLGIEGAPQSLSIKTSSLAEARNMADLIDGYCR 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 82; DB 1; Length 1009;
; Pred. No. 1e+02;
13; Mismatches 34; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein kinase activation.";
J. Biol. Chem. 271:29993-29998(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Ptk2b; Synonyms=Fak2, Pyk2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.9%;
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Best Local Similarity 26.9°
Matches 29; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
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TISSUE-Hippocampus;

MEDLINE-9811659; PubMed-9645946;

Xiong W.-C., Macklem M., Parsons J.T.;

Xiong W.-C., Macklem M., Parsons J.T.;

Repression and characterization of splice variants of PYK2, a focal adhesion kinase-related protein.";

J. Cell Sci. 111:1981-1991(1998).

J. Cell Sci. 111:1981-1991(1998).

J. Cell Sci. 111:1081 and activation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated receptors or neurotransmitters that increase calcium flux and the commercem signals that regulate neuronal activity. Interacts with the Styl domain of Grbz. May phosphorylate the voltage-gated potassium channel protein NV1.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its scontent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=2; Synonyms=PRUK;
Isold=P70600-2; Sequence=VSP_004982, VSP_004983;
Name=3; Synonyms=PRUK2;
Isold=P70600-2; Sequence=VSP_004984;
Isold=P70600-3; Sequence=VSP_004984;
TISSUE SPECIFICITY: Isoform 1 is expressed at high levels in the brain (hippocampus, cerebral cortex and olfactory bulb) and poorly in the spleen and other tissues, whereas isoforms 2 and 3 are expressed in the spleen and brain (hiphest in cerebellum).
PTM: Phosphorylated on tyrosine residues in response to various etimuli that elevate the intracellular calcium concentration, as well as by PKC activation. Recruitment by Nephrocystin to cell matrix adhesions initiates Tyr-402 phosphorylation (By emitiates Tyr-402 phosphorylation (By emitiates)
                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate. SUBUNIT: Interacts with PTPNS1 and DDEF2 (By similarity). Isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1, but not isotomm 2, interacts with Crk-associated substrate (Cas), Nephrocystin and OPHNIL.
SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin induces the membrane-association of the kinase (By similarity). Isoform 2 localizes to focal adhesions, but not isoforms 1 and 3. ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity). In monocytes, adherence to substrata is required for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphorylation and kinase activation. Angiotensin II, thapsigargin and L-alpha-lysophosphatidic acid (LPA) also induce autophosphorylation and increase kinase activity. SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
                         FROM N.A. (ISOFORMS 2 AND 3), SUBCELLULAR LOCATION, AND FAT
                                                                                                                                                                                                                                                                                                                                                                                        activity.
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=P70600-1; Sequence=Displayed;
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InterPro; IPR011009; Kinase like.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR001245; Tyr Dkinase.
InterPro; IPR008246; Tyr Dkinase AS.
Pfam; PP03623; Focal AT; I.
Pfam; PP03069; Pkinase; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR000299; Band 4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF063890; AAC28340.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U69109; AAC52895.1; -.
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HSSP; Q05397; 1K04.
RGD; 628758; Ptk2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR009065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               subfamily
[3]
SEQUENCE 1
                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
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88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDTKPTCLABFKQI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Different evolutionary processes shaped the mouse and human olfactory
                                                                                                                                                                                                                                                                                                                                                    Missing (in isoform 2).

/FTId=VSP 004982.

NVPKRHSMR -> MGLIVLSSQ (in isoform 2).
/FTId=VSP 004983.

Missing (In isoform 3).
/FTId=VSP 004984.

E -> A (in Ref. 2).
V -> F (in Ref. 3).

W -> F (in Ref. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGUENCE FROM N.A.
MEDLINE=21864068; PubMed=11875048;
Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
Trask B.J.;
                                                                                                                                                                                                                                                                 Focal adhesion targeting (FAT).
Phosphotyrosine (By similarity).
Phosphotyrosine (by autocatalysis) (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
        Probom, PD000001, Prot Kinase; 1.

SMART; SM00295; B41; 1.

SMART; SM00295; B41; 1.

SMART; SM00295; B41; 1.

PROSITE; PS00660; FERM 1; FALSE NEG.

PROSITE; PS00661; FERM 2; FALSE NEG.

PROSITE; PS00107; PROTEIN KINASE ATP; 1.

PROSITE; PS00109; PROTEIN KINASE TYP; 1.

PROSITE; PS00109; PROTEIN KINASE TYP; 1.

PROSITE; PS00109; PROTEIN KINASE TYP; 1.

PROSITE; PS01010; TANDSE TYP; 1.

PROSITE; PS01010; PROTEIN KINASE TYP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139 DSDHCFPLPAME-----EGATILVTTKTND------YCK 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein kinase.
ATP (By similarity).
ATP (By similarity).
Proton acceptor (By similarity)
                                                                                                                                                                                                                                                                                                                         Phosphotyrosine (By similarity)
Phosphotyrosine (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 1009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 27, Last annotation update)
01factory receptor MOR202-36 (Olfactory receptor Olfr1475).
Name=Olfr1475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21676863; PubMed=11802173;
Zhang X., Firestein S.;
"The olfactory receptor gene superfamily of the mouse.";
Nat: Neurosci. 5:124-133(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.5%; Score 82; DB 1;
26.9%; Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Mismatches
                                                                                                                                                                                                                                           Pro-rich
                                                                                                                                                                                                                                                        Pro-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1009 AA; 115784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.98;
PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 26.9
Les 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                     969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                579
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                                                                                                                                                                                 DOMAIN
NP BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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                                                                                                                                                                                                                                                                                                                                           4OD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OBVEV6;
                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                      DOMAIN
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Matches
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65 IISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDL----EKSRTGDEIILPRGLE 120
                                                                                                               6 GOCSONEYFDSLLHACIPCOLRCSSNTPPLTCORYCNA-SVTNSVKGTNAILWTCLGLSL
                                                                                                                                                                                                                                                                                         121 YTVEECTC----EDCIKSKPKVDSDHCFPLPAMEEGATI-----LVTTKTN 162
                                                                                                                                                                                                                                                                                                                                    YTVELČEAYKPSSNČV - - PNGTKKGČMELAAKCESRTIKEQCDVAGTKTN 651
                        Query Match 8.5%; Score 81.5; DB 2; Length 2233; Best Local Similarity 25.1%; Pred. No. 2.6e+02; Matches 43; Conservative 17; Mismatches 58; Indels 53
                                                                                                                                                                                                                                  562 TCSA-----LIVKENCELKANREK---CGWTGSTCVDIVCTTAPTKTDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=Columbia;
MEDLINE=93066369; PubMed=1438303;
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Matches 39; Conserva
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                                                                                                                                                                                                                                                                                                                                    604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CSQNEYFDSLLHACIP-CQLRCSSNT-----PPLTCQRYCNASVTNSVKGTNAILWT
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J. Mol. Biol. 222:835-841(1991).

J. Mol. Biol. 222:835-841(1991).

J. Mol. 228669; T28669.

Interpro; IPR002895; Paramecium SA.

Ffam; PF01309; Paramecium SA, 25.

SMART; SM00639; PARA, 26.

SEQUENCE 2233 AA; 237076 MW; C064FE0AF7BB873B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Alveolata, Ciliophora, Oligohymenophorea, Peniculida,
Paramecium.
                                                                                                                                                                                                                                                                                                                                                                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 81.5; DB 2; Length 314; 30.4%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Mismatches 40; Indels
                                                                                        Adams M.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                        Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 CDGILTLLVILNTYLLIFIAILRWRSAEAQRKAFSTCASHLI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 AA; 34996 MW; 9C7B11A5917EA632 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLG-LSLIISLAVFVLMF--LLRKISSEPLKDEFKNTGSGLL 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00245; OLFACTORYR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PS50262; G PROTEIN RECEP F1 2; 1.
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                        Hum. Mol. Genet. 11:535-546(2002)
                                                                                                                                                                                                                                                                                                      Genome Biol. 4:R71-R71(2003)
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Q94711;
01-FEB-1997 (TrEMBLrel, 02, (
^. - FER-1997 (TrEMBLrel, 02,
receptor gene families.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 30.4 tes 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paramecium tetraurelia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51C surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00001; 7tm
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                         expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Receptor.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                           Name-pro25;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith T.A., Kohorn B.D.; "An Arabidopsis serine threonine kinase homologue with an EGF repeat selected in yeast for its specificity for a thylakoid membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0005529; F:ATP binding; IEA.

R GO; GO:0005509; F:calcium ion binding; IEA.

R GO; GO:0006464; F:Protein serine/threonine kinase activity; IEA.

R GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR000152; Asx hydroxyl_S.

R InterPro; IPR000519; EGF_2.

R InterPro; IPR000529; EGF_like.

R InterPro; IPR000509; EGF_like.

R InterPro; IPR000519; Fort kinase.

R InterPro; IPR000511; Ser_Chinase.

R InterPro; IPR000511; Ser_Chinase.

R Pfam; PP00669; Pkinase: 1.

R Pfam; PP00669; Pkinase: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 89:10989-10992(1992).
-!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
EMBL; L04999; AAA32844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.4%; Score 81; DB 2; Length 595; 24.5%; Pred. No. 72; tive 27; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     595 AA; 65898 MW; 7B58FC1A656E0641 CRC64;
                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
595 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD000001; Prot_kinase; 1.
SMART; SM00179; EGF CA; 1.
PROSITE; PS00010; AŠX HYDROXYL; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 2.
PROSITE; PS50011; PROFIEIN KINASE DOM; 1.
PROSITE; PS001187; PSCOTEIN KINASE DOM; 1.
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304 SSLNCTSC--SSPTTISTNCAPIPAPADDKYFTPVSRTEARCIRLTRALNGQSGFGVRTQ 361
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Genome Biol. 4:R71-R71(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tonnes-Priddy L., Ross J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AY318691; AAP71834.1; -.
EMBL; AX318691; Cintegral to membrane; IEA.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0001894; F:receptor activity; IEA.
GO; GO:000186; P:G-protein coupled receptor protein signalin.
InterPro; IRRO0276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm 1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.4%; Score 80.5; DB 2; Length 314; 10.4%; Pred; No.41; Ve 16; Mismatches 40; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanders K.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               203 CDGILTLLVILNTYLLIFIAILRMRSVBAQRKAFSTCASHLI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 AA; 35001 MW; DF19DD033F8B2FD8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22974002; PubMed=14611657;
Young J.M., Shykind B.M., Lane R.P., T
Walker M., Williams E.M., Trask B.J.;
                                                                                                                                                                                                                                                                                                                                     Created)
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01-MAR-2003 (TrEMBLrel. 23,
01-JUN-2003 (TrEMBLrel. 24,
CG31262-PA.
ORFNames=CG31262;
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                                                                                                                                                                                                                                                                                                                                                                                                      Olfactory receptor Olfr1472.
Name=Olfr1472;
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Best Local Similarity 30.4%
Matches 31, Conservative
                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
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                                                                                                                                                1:::
362 IDQN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                    177 IEKS 180
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                                                                                                                              187 TMSCKRKBFAWTTILLVTTIGF-LVILLGVACIQQRMKHLKDTKLRBQFFBQNGGGMLTQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 PPKSNATCQGPPKSCSDPVHDRIRSITGYCNNRGKPTQANSVTAIRRLLGTTSYTDGLQA 243
                             CRCNBGFDGNPYLSAGCQDVNECTISSTIHRHNCSDPRICRNKVGGFYCKCQSGYRLDIT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISLAVFVLMFLLRKISSEPLKDEFKNTG-SGLLGMANIDLEKSRTGDEIILPRGLEYTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 IRNTSVIGSPLPSIRLISNKLHDEGSTPNFSPSVNHLHMQIGQFIAHDIIFMPSSIAKDG 303
CSQNEYFDSLLHACIPCQ--LRCSSN-----TPPLTCQR----YCNA----SV 45
                                                                                            TNSVK-----GTNAILWTCLGLSLIISLAVFVLMFLLRKISSEPLKDE-FKNTGSGLL--
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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21.7%; Pred. No. 95;
tive 25; Mismatches 91; Indels
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0457; ĀNPEROXIDASE.
PROSITE; PS50292; PEROXIDASE 3; 1.
Heme; Hypothetical protein; Īron; Oxidoreductase.
SEQUENCE 773 AA; 83992 MW; 4E3373FDA4EC67C7 CRC64;
                                                                                                                                                                                                                     246 RLSGPSNVDVKIFTEDGMKKATNGYAESRILGQGGGTV 284
                                                                                                                                                                                          -----LEKSRTG--DEIILPRGLEYTV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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WormPep; R08F11.7; CE12592.
GO; GO:0004601; F:peroxidase activity; IEA.
InterPro; IPR002007; Anim_peroxidase.
InterPro; IPR010255; Peroxidase super.
PF03098; An_peroxidase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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MEDLINE-99069613; PubMed-9851916;
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01-MAR-2004 (TrEMBLrel. 26, Le
Hypothetical protein ROBF11.7
ORFNames=ROBF11.7,
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PIR; D89010; D89010.
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Submitted (MAY-1997)
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Addams M.D. Celnikers S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Addams M.D. Celnikers S.E., Holt R.A., Forns C.A., Gocayne J.D.,
Adams M.D. Celnikers S.E., Hill R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
B. Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
An M. K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
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Bellew R.M., Bencs P.V., Berman B.P., Bandarib D., Bolshakov S.,
Berkova D., Botchen M.R., Bouck J., Brokstein P., Berchist P. M.,
Berkova D., Botchen M.R., Bouck J., Brokstein P., Berchist P. M.,
Borkova D., Botchen M.R., Bouck J., Brokstein P., Berchist P.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Abboron K., Doup L.E., Downes M., Dugarn-Rocha S., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Durkov B.C., Dunn P.,
Abboron K., Doup L.E., Downes M., Dugarn-Rocha S., Dunkov B.C.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Plaischman W.,
Rober C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Adlali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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Liasko P., Lei Y., Levitsky A.A., Li J.J., Li Z., Liang Y., Lin X.,
Allali M., Moy M., Murphy B., Murphy L., Murzny D.M., Nelson D.L.,
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Nelson D.K., Nolson K.A., Nikan M., Stupek M., Stur B.,
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Shier E., Spradling A.C., Pan S., Pollard J., Puri V., Sher M.,
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Sylersa R., Zhong W., Zhan M., Zhang G., Zhu X., Smith H.O.,
Alberner R., Zaveri J.S., Zhu K., Zhon S., Zhu X., Smith H.O.,
Steinec 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
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MEDLINE=22426069; Pubmed=12537572;
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                                                SEQUENCE FROM N.A.
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                 NCBI_TaxID=7227;
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311 SERQSTILIKTCI---IPQGILAFLIVFLLQHIRGILSVCNSISSITAGTSFGVFTLGML 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 368 FPWANTIGTAVGGLSSVLLAGWISFGSQIAAASGQLKSGMLPVSVKECVGNVTLPEDPWV 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 DQDQVFPLYRLSYHWVSPIGVVTAVVVGALVSLITKPAD-IKTLHAELISPVIHRSV 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 SVKGTNAILWTCLGLSLIISLAVFVLMFLLR------KISSEPLKDEF-----
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"A cluster of five cell wall associated receptor kinase genes, Wakl-5,
are expressed in specific organs of Arabidopsis.";
plant Mol. Biol. 39:1189-1196(1999).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kamiya J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Skinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
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Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47;
Annotation of the Drosophila melanogaster euchromatic genome:
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Wall-associated kinase 1 (Hypothetical protein At1g21250).
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                                                                                                                                                                                                                                                                                                                                                                                                                                       FIYBASE, FREGNO051262, GG31262.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

GO; FREGNIAS, P: TRANSPORT; IEA.

FREGNIAS; PS:0283; NA SOLUT SYMP 3; 1.

SEQUENCE 487 AA; 53156 MW; 454B1312B8CC2C9C CRC64;
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                                                                  Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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Best Local Similarity 23.74
Matches 42; Conservative
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                                          systematic review.";
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Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
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MEDLINE=22787088; PubMed=12204565;
MEDLINE=22787088; PubMed=12204565;
Desnoues N., Lin M., Guo X., Ma L., Carreno-Lopez R., Elmerich C.;
"Nitrogen fixation genetics and regulation in a Pseudomonas stutzeri
strain associated with rice.";
Microbiology 149:2251-2262(2003).
                                                                                                                                                                                                                   R EMBL; AJ009656; CAA608794.1; -
R EMBL; AJ009656; CAA608794.1; -
R EMBL; BT001967; AAA71966.1; -
R EMBL; BT001967; AAA71966.1; -
R EMSP; P01130; 1HZ8.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0006468; P:protein serine/threonine kinase activity; IEA.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
R InterPro; IPR000125; Asx_hydroxyl_S.
R InterPro; IPR001881; EGF_Z.
R InterPro; IPR001881; EGF_Z.
R InterPro; IPR001999; EGF_2.
R InterPro; IPR001999; EGF_2.
R InterPro; IPR001099; EGF_2.
R InterPro; IPR001099; EGF_2.
R InterPro; IPR001099; EGF_2.
R InterPro; IPR0011099; EGF_2.
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R InterPro; IPR0011099; EGF_2.
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R InterPro; IPR0011099; EGF_2.
R InterPro; IPR0011099; EGF_2.
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Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                    Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PSS0026; EGF_3; 2.
PROSITE; PS01187; EGF_CA; UNKNOWN 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS500118; PROTEIN KINASE ST; 1.
ATP-binding; EGF-11ke domain; Hypothetical protein; Kinase;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Avraham S., London R., Fu Y., Ota S., Hiregowdara D., Li J., Jiang S., Pasztor L.M., White R.A., Groopman J.B., Avraham H.;
"Identification and characterization of a novel related adhesion focal tyrosine kinase (RAFTK) from megakaryocytes and brain.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      014289; 013475; 014290; 016709; 15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUL-1998 (Rel. 36, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase 2) (FADK 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase beta) (CAK beta) (Calcium-dependent tyrosine kinase)
                                                                                                                                                                                                                                                                                                                                                 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Hippocampus; MEDINE-95403156; MEDINE-95403156; PubMed=7673154; MEDINE-95403156; PubMed=7673154; Sasaki H., Kotani K., Sasaki T.; Sasaki H., Nagura K., Ishino M., Tobioka H., Kotani K., Sasaki T.; "Cloning and characterization of cell adhesion kinase beta, a novel protein-tyrosine kinase of the focal adhesion kinase subfamily."; J. Biol. Chem. 270:21206-21219(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sutherland G.R., Shine J.; of FAK2, a novel human focal
                                                                                                                                                                                                                                                                              Length 153;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                               153 AA; 17188 MW; 0C849770A6EEA7C7 CRC64;
EMBL, AJ297529, CAD44480.1, -. GO, GO:0016846, F:carbon-sulfur lyase activity; IEA. GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                 35;
                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1009 AA.
                                                                                                                                                                                                                                                                              Score 79.5; I
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=PTK2B; Synonyms=FAK2, PYK2, RAFTK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 CPRCGSSVFARTADEIEVSLGA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 --- CKSLPAALSATEIEKSISA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Hippocampus;
MEDLINE=96435912; PubMed=8838818;
Herzog H., Nicholl J., Hort Y.J.,
Molecular cloning and assignment
adhesion kinase, to 8p11.2-p22 by
Genomics 32:484-486 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
MEDLINE=95379967; PubMed=7544443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adhesion focal tyrosine kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 32.9%;
Matches 27; Conservative
                                                                                                                                        Pfam; PF04828; DUF636; 1. Hypothetical protein.
                                                                                                                InterPro; IPR006913; GFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Event=Alternative splicing; Named isoforms=2;

IsoId=Q14289-1; Sequence=Displayed;

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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Nausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldow M.F., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Wishin T.B., Tooshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A. Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Schnerch A., Schain J.B., Jones S.J.M., Marra M.A.,
Scherztion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mass spectrometry.";

Proc. Natl. Acad. Sci. Us.A. 100:443-448 (2003).

Proc. Natl. Acad. Sci. Us.A. 100:443-448 (2003).

InvOlved in calcium induced regulation of ion channel and activation of the map kinase signaling pathway. May represent an important signaling intermediate between neuropeptide activated receptors or neurotransmitters that increase calcium flux and the downstream signals that regulate neuronal activity. Interacts with the SH2 domain of Grb2. May phosphorylate the voltage-gated potassium channel protein KV1.2. Its activation is highly correlated with the stimulation of c-Jun N-terminal kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andreev J., Simon J.-P., Sabatini D.D., Kam J., Plowman G.,
Randazzo P.A., Schlessinger J.;
"Identification of a new Pyk2 target protein with Arf-GAP activity.";
Mol. Cell. Biol. 19:2338-2350(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21396557; PubMed-11493697; DOI=10.1073/pnas.171269898; Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim B., Walz G.; Wiephrocystin interacts with Pyk2, pl30(Cas), and tensin and triggers phosphorylation of Pyk2."
                                      Li X., Hunter D., Morris J., Haskill J.S., Earp H.S., m.A calcium-dependent tyrosine kinase splice variant in human monocytes. Activation by a two-stage process involving adherence and subsequent intracellular signal.", J. Biol. Chem. 273:9361-9364(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=12522270; DOI=10.1073/pnas.2436191100; Salomon A.R., Ficarro S.B., Brill L.M., Brinker A., Phung Q.T., Existen C., Sauer K., Brock A., Horn D.M., Schultz P.G., Peters B.C., "Profiling of tyrosine phosphorylation pathways in human cells using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION SITE TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                             Blechschmidt K., Jandrig B., Baumgart C., Dette M.D., Jahn N., Menzel U., Schilhabel M.B., Wen G., Taudien S., Rosenthal A.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION SITES TYR-579 AND TYR-580.
MEDLINE=98211954; PubMed=9545257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WITH NEPHROCYSTIN.
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                     Isold=014289-2; Sequence=VSP 004981;
-1-TISSUE SPECIFICITY: Most abundant in the brain, with highest levels in anyddala and hippocampus. Low levels in Kidney. Also expressed in spleen and hippocampus. Low levels in Kidney. Also expressed in spleen and hippocampus. Low levels in Kidney. Also expressed in spleen and hippocampus. Low levels in kidney. Also stimuli that elevate the intracellular calcium concentration, as well as by PKC activation. Recruitment by Nephrocystin to cell matrix adhesions initiates Tyr-402 phosphorylation. In monocytes, adherence to substrata is required for tyrosine phosphorylation and kinase activation. Angiotensin II, thapsigargin and L-alphalysophosphatidic acid (LPA) also induce autophosphorylation and increase kinase activity (By similarity).
-!- SIMILARITY: Belongs to the Tyr family of protein kinases. FAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIM, 601212; -. Goytoplasm; TAS.

GO, GO:0005737; C:cytoplasm; TAS.

GO, GO:0004715; F:non-membrane spanning protein tyrosine kina. . .; TAS.

GO; GO:0004815; P:apoptcosis; TAS.

GO; GO:0006818; P:postein regulation of cell proliferation; TAS.

GO; GO:0006461; P:protein anino acid phosphorylation; TAS.

GO; GO:0006461; P:protein complex assembly; TAS.

GO; GO:0006950; P:response to stress; TAS.

GO; GO:0007172; P:signal complex formation; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Alternative splicing, ATP-binding; Phosphorylation; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein kinase.
ATP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0109; TYRKINAGE.
ProDom; PD000001; Prot_kinase; 1.
SMART; SM00295; B41; 1.
PROSITE; PS00650; FERM 1; FALSE NEG.
PROSITE; PS00661; FERM 2; FALSE_NEG.
PROSITE; PS00651; FERM 2; FALSE_NEG.
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS001107; PROTEIN KINASE_DOM; 1.
PROSITE; PS001109; PROTEIN KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 FERM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000299; Band 4.1.
InterPro; IPR0005189; PBRM
InterPro; IPR0015189; Proal AT.
InterPro; IPR011009; Kinase like.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase.
Pfam; PF03623; Pocal AT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF311103; -; NOT ANNOTATED_CDS.
EMBL; BC04259; AAH42599.1; -.
PIR; S60248; S60248.
HSSP; Q05397; 1K04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U33284; AAC50203.1; -. EMBL; L49207; AAB47217.1; -. EMBL; D45853; BAA08289.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U43522; AAC05330.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q05397; 1K04.
; HGNC:9612; PTK2B.
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                                                                                                                                                                                                                                                                                                                                                     subfamily
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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tyrosine phosphate. SUBUNIT: Interacts with Crk-associated substrate (Cas), PTPNS1 (By

CATALYTÎC ACTIVITY: ATP + a protein tyrosine = ADP + protein

similarity), Nephrocystin, DDEF2 and OPHNIL. SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin induces the membrane-association of the kinase.

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PD000001;
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       ACCOOOS SEED TO THE SEED TO THE SEED TO THE SEED TO THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE SEED THE S
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WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

WEDLINE-22388257; PubMed=12477932;

WEDLINE-22882; Locatellang F.S., Wanger L., Schaefer C.F., Bhat N.K.,

Norden M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., WcKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Raha S.S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakeley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                       88 EFKNTGSGLLGMANIDLEKSR-----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     15;
                                Proton acceptor (By similarity). Pro-rich. Pro-rich.
                                                                                                                                                                            Score 79.5; DB 1; Length 1009;
Pred. No. 1.7e+02;
9; Mismatches 29; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R., Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, BC036651; AAH36651.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) PTK2B protein tyrosine kinase 2 beta, isoform a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
       ATP (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1009 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR011009; Kinase_like.
InterPro; IPR000719; Prot Kinase.
InterPro; IPR001299; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
InterPro; IPR08266; Tyr_pkinase_AS.
Pfam; PF03623; Pocal AT; 1.
Pfam; PF00069; Pkinase; 1.
PRINTS; PR00109; TYRKINASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    306 RSIRCLPL---ÈEGQAVL 320
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InterPro; IPR000299; Band 4.1.
InterPro; IPR009065; FERM.
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                                                                                                                                                                            ch 8.2%;
l Similarity 32.1%;
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
          457
549
767
869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004
05-JUL-2004
BINDING
ACT SITE
DOMAIN
DOMAIN
                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                 Matches
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**X. Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., MEDLINE=2288257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., A Klausner R.D., Colling F.S., Wagner L., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Ditchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Bromalecin M.J., Usdin T.B., Tooshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Halton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Shevchenko X., Bouffard G.G., Schmutz J., Myers R.M., Butterfield Y.S., Narra M.A., Jones S.J., Marra M.A., Schmutz J., Myers R.M., Schein J.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Shalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Marra M.A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Schner E.D., Marra M.A., Schein J.E., Schner E.D., Marra M.A., Schein J.E., Schner E.D., Marra M.A., Schein J.E., Schner E.D., Marra M.A., Schein J.E., Schner E.D., Marra M.A., Schein J.E., Schner E.D., Marra M.A., Schein J.E., Schner E.D., Marra M.A., Schein J.E., Schner E.D., Schner E.D., Schner E.D., Schner E.D., Schner E.D., Schner E.D., Schner E.D., Schner E.D., Schner E.D., Schner E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               249 KFFNT---LAGFANIDQETYRCELIQGWNITVDLVIGPKGIRQLTSQDAKPTCLAEFKQI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 EFKNTGSGLLGMANIDLEKSR------TGDEIILPRGLEYTVEECTCEDCIKSKPKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Gaps
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Mammalia, Butheria, Primata, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1009;
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Pred. No. 1.7e+02;
9; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79.5; DB 2; Length 1
Pred. No. 1.7e+02;
9; Mismatches 29; Indels
                                  SMART; SM00295; B41; 1.
SMART; SM00210; S_TKC; 1.
SMART; SM00210; T_YRC; 1.
PROSITE; PS00107; FROTEIN KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN KINASE_DOM; 1.
ATP-binding; Kinase; Transferase.
SEQUENCE 1009 AA; 115906 MW; 58BABAA046274E7CZ CRC64;
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Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
PTX2B (TrEMBLrel. 27, Last annotation update)
PTX2B (Human).
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Prot_kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 RSIRCLPL---EEGQAVL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC036651; AAH36651.1;
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Best Local Similarity 32.1%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 32.1'
Matches 25, Conservative
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preliminary data
                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A.
  : | | |
--VEYSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=12368865;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=17XNL
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SEQUENCE 1
                          1260
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Q802S1;
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                                                                                                                                             Q7R6V0
                                                                                                 RESULT 44
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                                                                                                                     Q7R6V0
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1206 GALHTAPSADAAPSVAVVIIAVCAAAVGLFITVLVVLQAHSPREKKTRKTSVRG----- 1259
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----TGDEIILPRGLEYTVEECTCEDCIKSKPKV 138
                          TCLGLS------LIISLAV-----FVLMFLLRKISSEPLKDEFKNTGSGLLGMAN 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSONEYPDSLLHACIPCOLRCS----SNTPPLTCQRYCNAS----VTNSVKGTNAIL-W
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO, GO:0016620; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0008523; F:Peptidase activity; IEA.
GO; GO:0008289; F:subtilase activity; IEA.
GO; GO:0004714; F:rannmembrane receptor protein tyrosine kin.
GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
GO; GO:000508; P:protein amino acid phosphorylation; IEA.
GO; GO:0007169; P:pransmembrane receptor protein tyrosine kin.
InterPro; IPR000345; CytC, heme_BS.
InterPro; IPR006211; Furin-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.2%; Score 79.5; DB 2; Length 1299;
24.1%; Pred. No. 2.3e+02;
iive 26; Mismatches 48; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00190; CYTOCHROME C; UNKNOWN 3.
PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE ERF; 1.
Hydrolase; Protease; Serine protease.
SEQUENCE 1299 AA; 142019 MW; 4C3799C7BBC572AB CRC64;
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                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cieplik M., Klenk H.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ c
-! SIMILARITY: Belongs to peptidase family SB.
EMBL; ZGSB88; CAPA3116.1; -.
PIK; T42251; T43251.
                                                                                                                                                                                                                                                           1299 AA.
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InterPro; IPR009030; Grow Fac recept.
InterPro; IPR01031; Multiheem cyt.
InterPro; IPR000209; Pept 58 53.
InterPro; IPR000209; Pept 58 53.
InterPro; IPR00920; Prot inh propept.
InterPro; IPR002884; PrprotnconvertsP.
Pfam; PF00082; Peptidase 58; 1.
Pfam; PF01483; P. Dycprotein; 1.
PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                             Spodoptera frugiperda (Fall armyworm)
EFKNTGSGLLGMANIDLEKSR---
                                                                                                                            RSIRCLPL---EEGQAVL 320
                                                                                          139 DSDHCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAR-2004 (TrEMBLrel. 26, Endoprotease FURIN.
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nes 39; Conservative
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00723; SUBTII
SMART; SM00261; FU; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7108;
                                                                                                                                                                                                                                                                                                                                                                                                       Name=FURIN;
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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Q26489
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93 INSKEDNITDFYGSHINSCDKYKTEISELKNHYHDYGNYNYKGL----IDKRKDFLYMD 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelii yoelii."; Nature 419:512-519(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carlton J.M., Angluoli S.V., Suh B.B., Kooij T.W., Pertea M., Silva J.C., Ermolaeva M.D., Allen J.B., Selengut J.D., Koo H.L., Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L., Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V., Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M., Florens L., Yates F.R. III, Raine J.D., Sinden R.B., Harris M.A., Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B., Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R., Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium yoelii yoelii.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=73239;
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8.2%; Score 79; DB 2; Length 333;
Best Local Similarity 27.1%; Pred. No. 60;
Matches 57; Conservative 24; Mismatches 79; Indels
||| :::|| :::|
-----LPRIDVDFTV----LTSCTDQEGPVEYEH 1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AABLO1002953; EAA20383.1; -.
InterPro, IPR006477; Yir bir cir.
Pfam, PF06022; Cir Bir Yīr; I.
TIGRPAMS; TIGRO1596; yir-bir-cir Pla; 1.
SEQUENCE 333 AA; 39110 MW; A3D4B87FF16D7391 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fugu rubripes (Japanese pufferfish) (Takifugu rubripes)
                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                       PRELIMINARY;
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Name=PY07843;
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Genew, HGNC:18153; TNFRSF13B.
MIM; 604907; -.
GO; GO:0005887; C:integral to plasma membrane; TAS.
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                                                                                                                                                                                                                                                                                                                                                                            FUNCTION
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    77 LRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            578 LINKISARTLDDRVVNTAKSLVGRANVHTALSLVGYBADLRKAMQYVFGSTLVCDTLDNAK 637
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).
Name=TNFRSF13B; Synonyms=TACI;
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MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                   R GO; GO:0016020; Cmembrane; IEA.

R GO; GO:0016020; Cmembrane; IEA.

R GO; GO:0005524; C:nucleus; IEA.

R GO; GO:0005524; C:nucleus; IEA.

R GO; GO:0004009; F:ATP binding in IEA.

R GO; GO:0007059; P:Chromosome segregation; IEA.

R GO; GO:0007059; P:Chromosome segregation; IEA.

R GO; GO:0007059; P:Chromosome segregation; IEA.

R GO; GO:0007059; P:Chromosome segregation; IEA.

R GO; GO:0007059; P:Chromosome segregation; IEA.

R GO; GO:0007059; P:Chromosome segregation; IEA.

R InterPro; IPR001439; SMC_C;

R InterPro; IPR001439; SMC_C;

R Ffam; PF02483; SMC_C; 1.

R Ffam; PF02483; SMC_C; 1.

R Pfam; PF02463; SMC_N; 1.

R Probom; PD000006; ABC_transporter; 1.

R PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 von Buelow G.-U., Bram R.J.;
"NF-AT activation induced by a CAML-interacting member of the tumor necrosis factor receptor superfamily.";
Science 278:138-141(1997).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
etilnopterygii, Neopterygii, Taleostei, Euteleostei, Neoteleostei,
Acanthomorpha, Acanthopterygii, Percomorpha, Tetraodontiformes,
Tetradontoidea, Tetraodontidae, Takifugu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.2%; Score 79; DB 2; Length 1200; 12.3%; Pred. No. 2.3e+02; ve 8; Mismatches 36; Indels
                                                                                                                                                                      Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the ABC transporter family.
EMBL; AJ5343131; CAD58848.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1200 AA; 135735 MW; 524394FD948321EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                293 AA.
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                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                    NCBI_TaxID=31033;
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T13x HUMAN
AC 014836,
DT 28-FEB.
DT 28-FEB.
DT 08-JUL
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DB TUMOT 1
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKerran K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G., Antherefield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Abnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-AT, as well as activation of NF-Rapas B and AP-1. Involved in the similation of B- and T-cell function and the regulation of humoral immunity.

-!- SUBUNIT: Binds TRAP2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLG with its C-terminus.

-!- SUBCELLULAR LOCATION: Type III membrane protein.

-!- TISSUB SPECIFICITY: Highly expressed in spleen, thymus, small intestine and peripheral blood leukocytes. Expressed in resting·B-cells and activated T-cells, but not in resting T-cells.

-!- SIMILARITY: Contains 2 TRRE-Cys repeats.

-!- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20341628; PubMed=10880535; MEDLINE=20341628; PubMed=10880535; MEDLINE=20341628; PubMed=10880535; Mia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R., Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J., Meng S.Y., Boyle W.J., Hsu H.; Meng S.Y., Boyle W.J., Hsu H.; Ecceptor for TALL-1, a tumor necrosis factor family member involved in B cell regulation."; J. Exp. Med. 192:137-143(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802; Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.B.; humoral immunity."; and receptors BCMA and TACI: system for regulating humoral immunity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200; Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., LaFleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.; "Tumor necrosis factor (TNF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLyS."; J. Biol. Chem. 275:35478-35485 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse cDNA sequences.";
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Gaps

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYBL outstation-the Buropean Bioinformatics Institute. The surper are no restrictions on its use by non-profit institutions as long as its content is in no way
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

Bult C.J. White O. Olsen G.J. Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Scotton R.A., Mougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Pererson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hust R.A., Kaine B.P., Boordovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

Complete genome sequence of the methanogenic archaeon, Methanococcus
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AX073405; AAL61068.1; -
GQ; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0004872; F: receptor activity; IEA.

GO; GO:0001872; F: receptor activity; IEA.

GO; GO:0007186; P: GP: Protein coupled receptor protein signalin.

InterPro; IPR000275; GP: Rhodpsn.

InterPro; IPR000725; Olfact_receptor.
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"MjKL, a K+ Channel from M. jannaschii, mediates K+ uptake and R
sensitivity in B. coli.";
FEBS Lett. 547:165-169(2003).
-!- FWOKTION: Probable potassium channel protein.
-!- SUNCELULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: Contains 1 trkA/RCK domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%; Score 78.5; DB 2; Length 314; 30.4%; Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 CDGILTLLVILNTYLLIFIAILRMRSVEAQRKAFSTCASHLI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 CLG-LSLIISLAVFVLMF--LLRKISSEPLKDEFKNTGSGLL 97
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 314 AA; 34987 MW; DESCDDF63E3B2FD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                         Pfam; PF00001; 7tm_1; 1.
PRINTS; PR0023; GPCRHUDOPSN.
PRINTS; PR00245; OLFACTORYR.
PROSITE; PS00237; G PROTEIN RECEP F1 1; UNKNOWN 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-DUL-2004 (Rel. 44, Last annotation update)
OrderedLoctasNames=MJ1357;
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Q58752;
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Matches
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      HID DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC DD DAC D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92
                         GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
InterPro; IPR001368; TWFR c6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : : | | | | : : | : : | : : | : : | : : | 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFCRSLSCRKEQGKFYDHLLRDCISCASI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT--NAILWTCLGLSLI
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                                                                                                                                                                                   Extracellular (Potential).
Signal-anchor for type III membrane protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys 1.
TNFR-Cys 2.
By similarity.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                  PROSITE; P800652; TNFR NGFR 1; 1.
PROSITE; P850050; TNFR NGFR 2; FALSE NEG.
Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;
Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 293;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> L (in Ref. 2).
411799F3DE17A5EB CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
01factory receptor MOR202-16.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%; Score 78.5; D
19.9%; Pred. No. 59;
ttive 35; Mismatches
GO:0004872; F:receptor activity; TAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 QDH-----AMEAGSPVSTSPEPVETC 230
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MEDLINE=21676863; PubMed=11802173;
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MEDLINE=21864068; PubMed=11875048;
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Hum. Mol. Genet. 11:535-546(2002)
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31816 MW;
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62
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86
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128
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93
128
128
251
293 AA;
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Best Local Similarity
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SEQUENCE FROM N.A.
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166
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TRANSMEM
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REPEAT
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CARBOHYD
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QBVFW0

RESULT 47

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Adams M.;

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MEDLINE=2238825; PubMed=12477932; MEDLINE=2238825; PubMed=12477932; MEDLINE=2238825; PubMed=12477932; MEDLINE=2238825; PubMed=12477932; Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heishe F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C., A. Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzatne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Milling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Marka M., Touchman J.W., Gareen E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Schnerch A., Schein J.E., Marka M.A., Jones S.J., Marka M.A., R. Generation and initial analysis of more than 15,000 full-length human
                                                      100 ANIDLEKSRTGDEIILPRGLEYTVEECTCEDCIKSKPK-----VDSDHCFPLPAME 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 NRISSVSIFLYGPLGLPLILS------TWEQPMTTFFKDTSSLVDWKKYHLCMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 522;
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEOURNCE 522 AA; 58061 MW; C7A9100E2E10E9E1 CRC64;
                        100 ANIDLEKSRIGDEILLPRGLEYTVEECTCEDCIKSKPK----
                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0T-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ22531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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26.3%; Pred. No. 1.1e+02;
:ive 17; Mismatches 48;
                                                                                                                                                                                                                                                                                                            PRT,
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InterPro; IPR007110; Ig-like.
                                                                                                                               151 -EGATILVTTKTN 162
                                                                                                                                                                             289 IWGVYTĽLŤTHĽŇ 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequences."
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289 IWGVYTLLTHLN 301
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 VLMFL-----LRKISS--EPLKDEFKNTGSGLLGMA-----NIDLEKSRTGD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EII-----LPRGLEYTVEECTCEDCIKSKPKV------DSDHCF-PLPAMEEG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 NRISSVSIFLYGPLGLPLILS------TWEQPMTTFFKDTSSLVDWKKYHLCMI 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EYFDSLLHACI PCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLIISLAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 DYFTALYPSVI------TITTTGYGDFTPKTFLGRTLTVVYLCVGVGIVMYLFSL
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EMBL, AROZGIA4; BABI5387.1; -
InterPro; IPR007110; IG-like.

SEQUENCE 485 AA; 54051 MW; 4474E549ACD560C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                             transport; Transmembrane; Transport. Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Potential.
Cytoplamic (Potential).
Selectivity filter (By similarity)
61231B0C001B54C4 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%; Score 78.5; DB 1; Length 343; 20.4%; Pred. No. 69;
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                                                                                                                                                                                                                                                      Pfam; PF02080; TrkA_C; 1.
Pfam; PF02054; TrkA_C; 1.
Complete proteome; Ton transport; Ionic channel; Potassium;
Domasium channel; Potassium transport; Transmembrane; TransmemIn 1 7 Cytoplasmic (Potential).
TRANSMEM 8 28 Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Mismatches 48; Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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26.3%; Pred. No. 99;
                                                                                                                                                                                                     Interpro; IPR001622; K+channel pore.
Interpro; IPR006037; TrkAC.
Interpro; IPR003148; TrkA N.
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8883 MW;
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                                                                                                 EMBL; U67575; AAB99365.1; -. PIR; D64469; D64469.
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                                                                                                                                                    HSSP; O27564; 1LNQ.
TIGR; MJ1357; -
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Sequence 4, Al
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US-09-855-564-2
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US-09-854-864-11
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                                                                                                                                                                                              ; Search time 163.743 Seconds (without alignments) 405.985 Million cell updates/sec
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1: \cgn2_6/ptodata/1/pubpaa/PtoT BW PUB.pep:*

2: \cgn2_6/ptodata/1/pubpaa/PtoT BW PUB.pep:*

3: \cgn2_6/ptodata/1/pubpaa/RtoT BW PUB.pep:*

4: \cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

5: \cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*

6: \cgn2_6/ptodata/1/pubpaa/USO8_NEW PUB.pep:*

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10: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: \cgn2_6/ptodata/1/pubpaa/USO9_NEW PUB.pep:*

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15: \cgn2_6/ptodata/1/pubpaa/USIOP_PUBCOMB.pep:*

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Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-077-438-7
US-10-077-137-1
US-10-068-725-2
US-10-151-882-47
US-10-151-192-8
US-10-152-3634-27
US-10-152-3634-27
US-10-087-080-39
US-10-087-080-39
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Sequence 166150,
Sequence 141214,
Sequence 43, Appli
Sequence 8, Appli
                                                       Sequence 22, Appl
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Sequence 7, Appli
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                      Sequence 8, A
Sequence 2, A
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1 US-10-293-816-2

1 US-10-008-063-8

1 US-10-152-363A-2

1 US-10-268-951-22

5 US-10-258-368-1

5 US-10-618-797-4

7 US-10-742-634-7

7 US-10-742-634-7

7 US-10-742-634-7

6 US-10-264-237-2773

6 US-10-264-237-2773

6 US-10-477-963-166150

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6 US-10-278-368-8
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100.0%; Score 964; DB 13;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10077438
Publication No. US20020165156A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MacKay, Fabience
APPLICANT: Schneider, Pascal
APPLICANT: Tachopp, Jung
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Homeder, Pascal
APPLICANT: Hompson, Jeffrey
APPLICANT: Bopech RED S.A.
ITLE OF INVENTION: Immunoregulatory Agent
FILE REPERENCE: A000PCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT APPLICATION NUMBER: 06/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR PILING DATE: 1999-08-17
PRIOR PILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-18
SOFTWARE: FASTERQ for Windows Version 4.0
SEQ ID NOS: 8
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ORGANISM: homo sapien
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Best Local Similarity
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RESULT

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121 YTVECTCEDCIKSKPKVDSDHCFPLPAMEGGATILVTTKTNDYCKSLPAALSATEIEKS 180
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Sequence 7, Application US/10077438

Publication No. US202016518641

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MacKay, Fabienne
APPLICANT: Ambrose, Christine
APPLICANT: Tschopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Bloquen, Inc.
APPLICANT: Bloquen, Inc.
APPLICANT: Apotech R&D S.A.
TITLE OF INVENTION: Baff Receptor (BCWA), An
TITLE OF INVENTION: Baff Receptor (BCWA), An
TITLE OF INVENTION: Immunorgulatory Agent
FILE REFERENCE: A080FCT
CURRENT APPLICATION NUMBER: US/10/077,438
CURRENT APPLICATION NUMBER: 60/149,378
FRIOR APPLICATION NUMBER: 60/149,378
FRIOR FILING DATE: 1999-08-17
PRIOR FILING DATE: 2000-02-18
FRIOR FILING DATE: 2000-02-18
FRIOR APPLICATION NUMBER: 60/181,684
FRIOR FILING DATE: 2000-02-18
NUMBER: PERLING DATE: 2000-02-18
NUMBER: PERLING DATE: 2000-02-18
NUMBER: PERLING DATE: 2000-02-18
NUMBER: PERLING DATE: 2000-02-18
NUMBER: PERLING DATE: 2000-02-18
NUMBER: PERLING DATE: 2000-02-18
SEQ ID NO S: SEQ ID NOS: 8
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Sequence 1, Application US/10077137
Sequence 1, Application No. US2020172674A1
GENERAL INFORMATION:
APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Biogen, Inc.
APPLICANT: Hompson, Jeffrey
APPLICANT: Apotech ReD S.A.
TITLE OF INVENTION: Immunoregulatory Agent
FILE REFERENCE: A000CT
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
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ORGANISM: homo sapien
US-10-077-438-7
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PUblication No. US20030059862A1
GENERAL INFORMATION
TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
FILE REPERENCE: P9554
CURRENT APPLICATION NUMBER: US/10/151,882
CURRENT FILING DATE: 2002-05-22
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 48
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Sequence 2, Application US/10068725

Sequence 2, Application US/10068725

Publication No. US20030012783A1

GENERAL INFORMATION:

TITLE OF INVENTION: Antibodies That Bind Both BCMA and TACI

FILE REFERENCE: 01-04

CURRENT APPLICATION NUMBER: US/10/068,725

CURRENT FILING DATE: 2002-02-06

PRIOR FILING DATE: 2001-02-20

PRIOR FILING DATE: 2001-04-12

PRIOR FILING DATE: 2001-04-12

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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100.0%; Pred. No. 2.7e-90;
tive 0; Mismatches 0;
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APPLICANT: Machopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Schneider, Pascal
APPLICANT: Schneider, Pascal
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Boggen, Inc.
APPLICANT: Baggen, Inc.
TITLE OF INVENTION: Baff Receptor (BCMA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE REPERBANCE: A080ECT
CURRENT APPLICATION NUMBER: US/10/077,137
CURRENT APPLICATION NUMBER: 06/149,378
PRIOR FILING DATE: 1999-08-17
PRIOR PILING DATE: 2000-02-15
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 184
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Best Local Similarity 100.
Matches 184; Conservative
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ORGANISM: homo sapien
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US-10-077-137-7
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; Publication No. US20030103986A1
; GENERAL INPORMATION:
; APPLICANT: Rixon, Mark W.;
; APPLICANT: GEOSS, Jane A.
; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins
; FILE REFERENCE: 01-20
; CURRENT APPLICATION NUMBER: US/10/152,363A
; CURRENT FILING DATE: 2002-05-20
; PRIOR PILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2.7
                   APPLICANT: Gross, Jane A.
APPLICANT: Xu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REFERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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; Pred. No. 2.7e-90;
0; Mismatches 0;
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Best Local Similarity 100.
Matches 184; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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                                         100.0%; Score 964; DB 14; Length 184; 100.0%; Pred. No. 2.7e-90; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 184;
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100.0%; Pred. No. 2.7e-90;
ive 0; Mismatches 0;
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                                    Query Match
Best Local Similarity 100.
Matches 184; Conservative
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ORGANISM: homo sapiens
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US-10-151-882-47
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US-10-115-192-8
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Indels

Length 184;

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APPLICANT: Yeh, Ren-Hwa
APPLICANT: Galperina, Olga
APPLICANT: Galperina, Olga
APPLICANT: Hibbert, David
APPLICANT: Hibbert, David
APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses The FILE REFERENCE: 1488.1810002
CURRENT APPLICATION NUMBER: US/10/742,634
CURRENT FILING DATE: 2003-12-22
PRIOR FILING DATE: 2002-12-33
PRIOR FILING DATE: 2003-05-02
RIOR APPLICATION NUMBER: US 60/467,198
PRIOR FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                       OTHER INFORMATION: tumor necrosis factor receptor superfamily, member OTHER INFORMATION: 17 (TNFRSF17)
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Publication No. US20040208824A1
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 39
LENGTH: 184
TYPE: RAT
ORGANISM: Homo sapiens
FEATURE:
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GENERAL INFORMATION:
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APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Mack, David H.

APPLICANT: Case Western Reserve University

TITLE OF INVENTION: No. US20030235820A1e1 Methods of Diagnosis of Metastatic Colorect

TITLE OF INVENTION: Cancer, Compositions and Methods of Screening for

TITLE OF INVENTION: Modulators of Metastatic Colorectal Cancer

FILE REFERENCE: 018501-000840US

CURRENT APPLICATION NUMBER: US 60/22,206

PRIOR FILING DATE: 2002-10-25

PRIOR FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: US 60/281,149

PRIOR APPLICATION NUMBER: US 60/281,149

PRIOR APPLICATION NUMBER: US 60/284,555
                                                                                                                                                                                                                  Sequence 11, Application US/10216074

Publication No. US20030148445A1

Fublication No. US20030148445A1

GENERAL INFORMATION:

APPLICANT: Shu, Hong-Bing

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

FILE REPERROCE: 2879-72

CURRENT APPLICATION NUMBER: US/10/216,074

CURRENT FILING DATE: 2000-05-05

FRIOR PELLING DATE: 2000-05-05

FRIOR PELLING DATE: 1999-05-06

NUMBER OF SEQ ID NOS: 17

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       121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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100.0%; Score 964; DB 14;
Best Local Similarity 100.0%; Pred. No. 2.7e-90;
Matches 184; Conservative 0; Mismatches 0;
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; ORGANISM: Homo sapiens
US-10-216-074-11
                                                      181 ISAR 184
                                                                                               181 ISAR 184
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US-10-216-074-11
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Sequence 11, Application US/09854864

Sequence 11, Application US/09854864

Sequence 11, Application US/09854864

GENERAL INFORMATION:

APPLICANT: THELL, LARS EXDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-668B

CURRENT FILING DATE: 2001-09-11

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR PEDICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

SPRIOR FILING DATE: 2000-05-12

SPRIOR FILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Version 3.1

SEQ ID NO 11
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                                                            98.5%; Score 950; DB 9; 1
100.0%; Pred. No. 7.1e-89;
.ive 0; Mismatches 0;
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; Publication No. US20020086018A1
                                                          Query Match
Best Local Similarity 100.
Matches 181; Conservative
    ; ORGANISM: Homo sapiens
US-09-855-158-5
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; TYPE: PRT
; ORGANISM: Murine
US-09-854-864-11
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US-09-855-158-11
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Sequence 5, Application US/09855158

Publication No. US20020086018A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: THELL, LARS EYDE

TITLE OF INVENTION: AND TACI

FILE OF INVENTION: AND TACI

FILE OF INVENTION: 3, AND TACI

FILE OF INVENTION: 3, AND TACI

FILE OF INVENTION: 3, AND TACI

FILE OF INVENTION: B. S. O01-09-11

FILE OF INVENTION: B. S. O01-09-11

FILE OF INVENTION: APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-06-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin version 3.1

SEQ ID NO 5

LENGTH: 181

TYPE: PRI
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121 YTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKS 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 BECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCKSLPAALSATEIEKSISA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLFCQRYCNASVTNSVKGTNAILWTCLGLS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS
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7.1e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.5%; Score 950; DB
100.0%; Pred. No. 7.1
:ive 0; Mismatches
                                                                                                                                                                        Sequence 5, Application US/09854864
Patent No. US20020081296A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                      181 ISAR 184
                                                                          181 İSAR 184
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APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
TITLE OP INVENTION: 3, AND TACI
FILE REFERENCE: A-666A
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENTIN Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPRENCE: A-666E
CURRENT PELING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-13
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
                                                   119
                                                                        120 BYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
                                                                                                                                                                     8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLSLI 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSONEYPDSLLHACIPCOLRCSSNTPPLTCORYCNASVTNSVKGTNAILWTCLGLSLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Pred. No. 2.3e-25; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 323; DB 9;
Pred. No. 2.3e-25
                                                64 LIISLAVFVLMFLLRKISSEPLKDEFKN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/09855158 Publication No. US20020086018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 21, Application US/09854864
Patent No. US20020081296A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 33.5%;
Best Local Similarity 100.0%;
Matches 58; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: THEILL, LARS EYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                  178 EKSISAR 184
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Best Local Similarity
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                                                          APPLICANT: YU, GANG
TITLE OF INVENTION: 3, AND TACI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shu, Hong-Bing
TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 2879-72
CURRENT APPLICATION NUMBER: US/10/216,074
CURRENT FILING DATE: 2003-03-12
PRIOR PILING DATE: 2000-05-05
PRIOR PILING DATE: 2000-05-05
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 1999-05-06
PRIOR PILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 LIISLAVFVLMFLLRKISSEPLKDEFKN----TGSGLLGMANIDLEKSRTGDEIILPRGL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 EYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDYCK-SLPAAL-SATEI 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 EYTVEECTCEDCVKSKPKGDSDHFFPLPAMEEGATILVTTKTGDYGKSSVPTALQSVMGM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGTYTVLWIFLGLT 58
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Pred. No. 3.4e-50;
21; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.3%; Score 572; DB 9; 62.6%; Pred. No. 3.4e-50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Mismatches
                                                                                                                              CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-06-27
PRIOR PILING DATE: 2000-06-27
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-05-12
SUFFWARE: PATENT NOWER: 1000-05-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PATENT VERSION 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17, Application US/10216074 Publication No. US20030148445A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.3%;
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 62.64
Matches 117; Conservative
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Best Local Similarity 62.6
Matches 117; Conservative
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ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 EKPTHTR 185
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ORGANISM: Murine
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Sequence 9, Application US/09854864
Sequence 9, Application US/09854864
Batent No. US20020081296A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS EXDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHADS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
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                                                                                                                                                       69 AVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEIILPRGLEYTVEECTC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLEKSRTGDEILLPRGLE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 VT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 YTVEECTCEDCIKSKPKVDSD-----HCFPLPAMEE-----GATILVTTKTNDY-- 164
                                                                                            2 AQCEYFDSLLHAC-PC-LRCS---PPTCQ-YC--SVT-SVKGT---LW--LGL---LSL 43
                                                                                                                                                                             44 A----FFILIRK----ELKDE------GSLAL------RGD---1PR-LEYTVEECTC 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 MLQMAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGVDK-THTC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----PPC----PAPELLGGPSVFLFPPKPKDTLMISKTPE
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                        49; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 302;
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/10115192
Publication No. US20030082175A1
GENERAL INFORMATION:
APPLICANT: Apotech R & D S.A.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: April Receptor (BCMA) and Uses Thereof
FILE REFERENCE: A0039CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Indels
                                                                                                                                                                                                                                                                 61.5%; Pred. No. 8.4e-24;
tive 4; Mismatches 7;
                                                                                                                                                                                                                                        129 EDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
29.7%; Score 286.5; DB
Best Local Similarity 39.9%; Pred. No. 1e-20;
Matches 81; Conservative 13; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/115,192
CURRENT FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/215688
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: 60/181807
PRIOR APPLICATION NUMBER: 60/157933
PRIOR PILING DATE: 1999-10-06
NUMBER: OF EQ. ID NOS: 12
SEQ. ID NO 12
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                      96; Conservative
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  Best Local Similarity
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                        Matches
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                                                                                                                                                                                                                                                   APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARG EYDE
APPLICANT: THEILL, LARG EYDE
APPLICANT: THEILL, LARGE
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERBNCE: A-686B
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR PLILING DATE: 2000-05-12
PRIOR PLILING DATE: 2000-05-12
PRIOR PLILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIN VERSION 3.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: 3, AND TACI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AQCEYFDSLIHAC-PC-LRCS----PPTCQ-YC--SVT-SVKGT---LW--LGL---LSL 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
                                                                     CSQNEYFDSLIHACIPCOLRCSSNTPPLICORYCNASVINSVKGINAILWTCLGLSLI 58
  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 311.5; DB 9; Dec. No. 8.4e-24; Indels
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDCIKSKPKVDSDHCFPLPAMEEGATILVTTKTNDY 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDC-KSKPK-DSDH-PPLPAMEEGATILVTTKT-DY 108
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
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CURRENT APPLICATION NUMBER: US/09/855,158
CURRENT FILING DATE: 2001-09-11
PRIOR PRILAMON NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-12
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin version 3.1
SECTION 117
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                                                                                                                                                                                           Sequence 12, Application US/09854864
Patent No. US20020081296A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 12, Application US/09855158; Publication No. US20020086018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: human-murine Consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: human-murine Consensus
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l Similarity 61.5%;
96; Conservative 4
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58; Conservative
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Matches 96; Conserve
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                                                                                                                                                                                                                                      GENERAL INFORMATION:
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Sequence 6, Application US/09854864

Sequence 6, Application US/09854864

Sequence 6, Application US/09854864

GENERAL INFORMATION:

HAPPLICANT: THERILL, LARS EVDE

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

TITLE OF INVENTION: UNMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/204,039

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-06-27

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PATENTING NOS: 31

SEQ ID NO 6

FRANCE SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-855-158-6

| Sequence 6, Application US/09855158 |
| Publication No. US2020086018A1 |
| Sequence 6, Application No. US2020086018A1 |
| Sequence 6, Application No. US2020086018A1 |
| GENERAL INFORMATION: APPLICANT: THEILL, LARS EYDE |
| APPLICANT: THEILL, LARS EYDE |
| APPLICANT: THEILL, LARS EYDE |
| TILE OF INVENTION: BITHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G770, BCMA, BL |
| TILE OF INVENTION: 3, AND TACI |
| FILE REFERENCE: A-686A |
| CURRENT FAPILICATION NUMBER: US/09/855,158 |
| CURRENT FILING DATE: 2001-09-11 |
| PRIOR APPLICATION NUMBER: US 60/214,591 |
| PRIOR APPLICATION NUMBER: US 60/204,039 |
| PRIOR PILING DATE: 2000-06-12 |
| PRIOR FILING DATE: 2000-05-12 |
| PRIOR FILING DATE: 2000-05-12 |
| SOFTWARE: PatentIn version 3.1 |
| SEQ ID NO 6
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1. Similarity 100.0%; Pred. No. 1.9e-21;
51; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 1.9e-21;
Matches 51; Conservative 0; Mismatches 0;
                                                                          VITKTNDY-----CKSLPAALSATEIEKSIS 182
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ORGANISM: Homo sapiens
US-09-855-158-6
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Best Local Similarity
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; Sequence of Application US/0985158
; Publication No. US2002086018A1
; GENERAL INFORMATION:
    APPLICANT: THEILL, LARS EYDE
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: TW. GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APPLICATION
; TITLE OF INVENTION: 3, AND TACI
; TILLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT APPLICATION NUMBER: US 60/214,591
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR PLING DATE: 2000-06-27
; PRIOR PLING DATE: 2000-05-12
; NUMBER OF SEC ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NOS: 30
; SEQ ID NOS: 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 DILMISKIPEVI----CVVVDVSHEDPEVKFNWYVDGVEVHNAKIKPREEQYNSIYRVVSV 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52 ------GGGGDKTHTCPPCPAPELLGGPSVFLFPPKPK 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 MAGQCSQNEYPDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
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                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.7%; Score 286; DB 9; Length 283; Best Local Similarity 37.6%; Pred. No. 1e-20; Matches 80; Conservative 12; Mismatches 47; Indels
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29.7%; Score 286; DB 9; Length 283;
Best Local Similarity 37.6%; Pred. No. 1e-20;
Matches 80; Conservative 12; Mismatches 47; Indels
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CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VETSION 3.1
                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-864-9
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| Sequence 7, Application US/09854864
| Patent No. US20020081296A1
| GENERAL INFORMATION:
| APPLICANT: THEILL, LARS EXDE
| APPLICANT: THEILL, LARS EXDE
| APPLICANT: THEILL, LARS EXDE
| APPLICANT: THEILL, LARS EXDE
| TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
| FILE REFERENCE: A-6868
| CURRENT FILING DATE: 2001-09-11
| PRIOR PRILICATION NUMBER: US 60/204,039
| PRIOR PPLICATION NUMBER: US 60/214,591
| PRIOR FILING DATE: 2000-06-27
| NUMBER OF SEQ ID NOS: 31
| SOFTWARE: Patentin Version 3.1
| SOFTWARE: Patentin Version 3.1
| TENNIC 24
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APPLICANT: THEILL, LARS EXDE

APPLICANT: THEILL, LARS EXDE

APPLICANT: THEILL, LARS EXDE

APPLICANT: THEILL, LARS EXDE

APPLICANT: W. GANG

TITLE OF INVENTION: 3, AND TACI

TITLE OF INVENTION: 3, AND TACI

TITLE OF INVENTION: 3, AND TACI

TITLE OF INVENTION: 3, AND TACI

TITLE OF INVENTION: MUMBER: US/09/855,158

CURRENT FILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-06-27

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-05-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE: PATENTIN VERSION 3.1

SEQ ID NO 7
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                                                                                                                                              28;
                                                                                         Length 207;
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                                                                                                                                                 Indels
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                                                                                   Score 264; DB 13;
Pred. No. 1.2e-18;
2; Mismatches 0;
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20.9%; Score 201; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.6e-13;
Matches 34; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                            1 MLQMAGQCSQNEYFDSL----
                                                                                   Query Match 27.4%;
Best Local Similarity 63.9%;
Matches 53; Conservative
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US-09-854-864-7
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; ORGANISM: homo sapien
US-10-077-137-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-09-855-158-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 264; DB 13; Length 207;
Pred. No. 1.2e-18;
2; Mismatches 0; Indels 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Browning Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Tachopp, Jurg
APPLICANT: Tachopp, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
APPLICANT: Biogen, Inc.
TITLE OF INVENTION: Baff Receptor (BCWA), An
TITLE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION: Immunoregulatory Agent
FILE OF INVENTION: 1909CT
CURRENT APPLICATION NUMBER: 60/149,378
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR PLLING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
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PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
PRIOR FILING DATE: 2000-02-11
                                                                                                                                  APPLICANT: Browning, Jeffrey
APPLICANT: Ambrose, Christine
APPLICANT: Technopy, Jurg
APPLICANT: Thompson, Jeffrey
APPLICANT: Thompson, Jeffrey
APPLICANT: Biogen, Inc.
APPLICANT: Apotech R&D S.A.
ITILE OF INVENTION: Baff Receptor (BCMA), An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/183,536
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: A080PCT
CURRENT PEPLICATION NUMBER: US/10/077,438
CURRENT FILING DATE: 2002-02.18
PRIOR APPLICATION NUMBER: 60/149,378
PRIOR PILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/181,684
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 CNASVTNSVKGQRYCNASVTNSV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 CNASVTNSVKG-----TNAI 55
                           Sequence 3, Application US/10077438
Publication No. US20020165156A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10077137
Publication No. US20020172674A1
GENERAL INFORMATION:
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                                                                                                                  APPLICANT: MacKay, Fabienne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 27.4
Best Local Similarity 63.9
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-077-438-3
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Length 34;

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Sequence 10, Application US/09855158

Publication No. US20020086018A1

GENERAL INPORMATION:
GENERAL INPORMATION:
JAND TACI

TITLE OF INVENTION:
FILE OF INVENTION:
FILE REPERBENCE: A-686A

CURRENT APPLICATION NUMBER: US/09/855,158

CURRENT PILING DATE: 2000-09-11

PRIOR PILING DATE: 2000-06-27

PRIOR PILING DATE: 2000-06-27

PRIOR PILING DATE: 2000-06-12

NUMBER OF SEQ ID NOS: 30

SOFTWARE PARENT NOS: 30

SOFTWARE PARENT NOS: 30

SEQ ID NO 10

SEQ ID NO 10
                                                                                                                                                                                       APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: METHODS AND TACI
FILE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERRINCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2000-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SOFTWARE: PATENTIN VERSION 3.1
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 PKDTLMISRTPEVT---CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVV 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 TGDEIILPRGLEYTVEECTCEDCIKSKPKVDSD-----HCFPLPAMEE-----GAT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.4%; Score 187; DB 9; Length 281; 29.8%; Pred. No. 1.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 187; DB 9;
Pred. No. 1.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSG-
                                                                                            Sequence 10, Application US/09854864 Patent No. US20020081296A1 GENERAL INFORMATION:
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                                                                                                                                                                        APPLICANT: THEILL, LARS EYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 29.8%
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Mus musculus
US-09-855-158-10
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Best Local Similarity
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; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: TY, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; TITLE OF INVENTION: 3, AND TACI
; TITLE OF INVENTION: 3, AND TACI
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; CURRENT APPLICATION NUMBER: US 60/214,591
; PRIOR PLING DATE: 2000-06-27
; PRIOR PLING DATE: 2000-06-27
; PRIOR PLING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 13
                                                                                                                                                                                                                                              Sequence 13, Application US/09854864

Sequence 13, Application US/09854864

Sequence 13, Application US/09854864

GENERAL INFORMATION:

APPLICANT: THELLA LARS EXDE

APPLICANT: YU, GAMP

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRLL/G70, BCMA,

TITLE OF INVENTION: BLYS/AGP-3, AND TACI

FILE REFERENCE: A-6868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT FILING DATE: 2000-05-12

PRIOR APPLICATION NUMBER: US 60/204,039

PRIOR APPLICATION NUMBER: US 60/214,591

PRIOR APPLICATION NUMBER: US 60/214,591

SPIOR APPLICATION NUMBER: US 60/214,591

SOFTWARE: Patent In version 3.1

SOFTWARE: Patent In version 3.1

SEQ ID NOS: 31

SEQ ID NO 13
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                                                    Indels
20.9%; Score 201; DB 9; I
100.0%; Pred. No. 3.6e-13;
tive 0; Mismatches 0;
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20.9%; Score 201; DB 9;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                             1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
Query Match 20.9
Best Local Similarity 100.
Matches 34; Conservative
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; ORGANISM: Consensus
US-09-854-864-13
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ORGANISM: Consensus
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US-09-855-158-13
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Gaps

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57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
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                                                                            21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80
                                               ----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 ÓCNÓTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALÓPQEGSALRPDVALLVGAPÁLL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 OCSONEYFDSLLHACIPCOL-----RCSSNTPPLTCQRYCNASVTNSVK---GINAIL
  35;
                                                                                                                                                                                                                                                          ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
                                                                                                                                                                                                                                112 BIILPRGLEYTVEECTCEDCIKSKPKVDSDHCFPLPAMEEGATILVTTKT 161
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                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/10380703
; Publication No. US20040072188A1
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc.
; APPLICANT: Thompson, Jeffrey S
; APPLICANT: Thompson, Jeffrey S
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
; FILE REFERENCE: BIOG-0086
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: 60/233,152
; PRIOR PILING DATE: 2000-09-18
; PRIOR PILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-02-13
; PRIOR PILING DATE: 2001-02-13
; PRIOR FILING DATE: 2001-02-13
; RING PILING DATE: 2001-02-13
; RING PILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIN Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 116.5; DB 15; Length 175; 29.4%; Pred. No. 0.0012; ive 21; Mismatches 64; Indels 35;
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Sequence 1, Application US/10469420

Publication No. US20040170997A1

GENERAL INFORMATION:

TITLE OF INVENTION: TRAF3-BINDING B-CELL-SPECIFIC RECEPTOR

TITLE OF INVENTION: TRAF3-BINDING B-CELL-SPECIFIC RECEPTOR

CURRENT APPLICATION NUMBER:

CURRENT FILING DATE: 2003-08-28

NUMBER OF SEQ ID NOS: 2

SOFFWARE: Patent In V2.1

SEQ ID NO 1
64; Indels
  Mismatches
21;
                                               7 QCSQNEYFDSLLHACIPCQL--
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Best Local Similarity 29.4*
Matches · 50; Conservative
  50; Conservative
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US-10-380-703-9
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  Matches
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US-10-145-206-197

Sequence 197, Application US/10145206

Publication No. US20030195156A1

GENERAL INFORMATION:

APPLICANT: MIN, HOSUNG

APPLICANT: APPLICANT: ZIONG, FEI

TITLE OF INFORMATION PERTIDES AND RELATED MOLECULES THAT BIND TO TALL-1

FILE REFERENCE: A-743

CURRENT FILING DATE: 2002-05-13

PRIOR APPLICATION NUMBER: US 60/290,196

PRIOR APPLICATION NUMBER: US 60/290,196

PRIOR APPLICATION NUMBER: US 60/290,196

NUMBER OF SEQ ID NOS: 197

SOFTWARE: Patentin version 3.1

SEQ ID NO 197

LENTH: 42
                                                                                                                                     64 LIISLAVFVLMFLLRKISSEPLKDEFKNTGSG-------LLGMANIDLEKSR 108
                                                                                                                                                                                                                                                             4 MAGQCSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGTNAILWTCLGLS 63
  Gaps
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                                                                                        1 MAQQCFHSEYFDSLLHACKPCHLRCSN--PPATCQPYCDPSVTSSVKGS--
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APPLICANT: Xu, Wenfeng
APPLICANT: Tu, Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Grant, Francis, J.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REPERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SEQ ID NO 13
LENGTH: 175
54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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100.0%; Pred. No. 1.2e-08;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    138 SVLTVLHODWLNGKEYKCKVSNKALPA-PIEKTIS 171
                                                                                                                                                                                                                                109 TGDEIILPRGLEYTVEECTCEDCIKSKPKVDSD-
  64; Conservative 17; Mismatches
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29.4%;
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Best Local Similarity 100.
Matches 28; Conservative
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Best Local Similarity
                                                                                                                                                                                   48 -----
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ORGANISM: Human
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; ORGANISM: Mouse
US-10-008-063-13
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53 ----NAILW---TCLGLSLIISLAVFVLMFLLRKISSEPLKDEFKNTGSGLLGMANIDLE 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 KSRTGDEILLPRGLEYTV--EECTCEDCIKSKPKVDSD-----HCFPLPAMEEGATIL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CVPTECYDLIARKCVDCRLIARKS--PPKTA----AGASSPAPGTALQPQESVGTGSGEV 71
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APPLICANT: Biogen, Jeffrey S
APPLICANT: Thompson, Jeffrey S
TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
FILE REPRENCE: BIOG-0086
CURRENT APPLICATION NUMBER: US/10/380,703
CURRENT FILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: 60/233,152
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-11
PRIOR PILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR PILING DATE: 2001-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/10251947
Publication No. US20030099990A1
GENERAL INFORMATION:
APPLICANT: Heu, Hailing
TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
FILE REFERENCE: 01-1160-A
CURRENT APPLICATION NUMBER: US/10/251,947
CURRENT PILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.4%; Score 100; DB 14; Length 185; Best Local Similarity 23.8%; Pred. No. 0.065; Matches 44; Conservative 25; Mismatches 62; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYCNASVTNSVKGT-----
                                                                                                                                                   Query Match 10.8%; Score 104; DB 9; Length 21; Best Local Similarity 100.0%; Pred. No. 0.0016; Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                               55 ILWTCLGLSLIISLAVFVLMF 75
                                                                                                                                                                                                                                                                                               1 ILWTCLGLSLIISLAVFVLMF 21
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; SEQ ID NO 8
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-8
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ORGANISM: Homo sapiens
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US-10-380-703-5
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; Sequence 8, Application US/09854864
; Patent No. US20020081296A1
; GENERAL INPORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI
; FILE REFERENCE: A-6868
; CURRENT APPLICATION NUMBER: US/09/854,864
; CURRENT FILING DATE: 2000-09-11
; PRIOR PILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-05-12
; PRIOR FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PATENTIN VERSION 3.1
; SOFTWARE: PATENTIN VERSION 3.1
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Publication No. US20020086018A1
GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: 3, AND TACI
FILE REFERENCE: A-666A
CURRENT APPLICATION NUMBER: US/09/655,158
CURRENT PILING DATE: 2000-06-27
PRIOR PILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
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                                                                                                                                                                                                                                                                                                                                        57 WTCLGLSLI--ISLAVFVLMFLLRKIS---SEPLKDEFKNTGSGLLGMANIDLEKSRTGD 111
                                                                                                                                                                                                                                 7 QCSQNEYFDSLLHACIPCQL-----RCSSNTPPLTCQRYCNASVTNSVK---GTNAIL 56
                                                                                                                                                                                                                                                                  21 QCNQTECFDPLVRNCVSCELFHTPDTGHTSSLEPGTALQPQEGSALRPDVALLVGAPALL 80
                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 ----PHASAPTWPPLK-EDADSALPR----HSVPVPATELGSTELVTTKT 170
                                                                                                                                                                                    35;
                                                                                                                              12.1%; Score 116.5; DB 16; Length 175; 29.4%; Pred. No. 0.0012; Live 21; Mismatches 64; Indels 35;
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                                                                                                                                                      Best Local Similarity 29.49
Matches 50; Conservative
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; ORGANISM: Homo sapiens
US-09-854-864-8
                        ; TYPE: PRT
; ORGANISM: Mouse
US-10-469-420-1
  LENGTH: 175
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PRIOR FILING DATE: 2001-08-14

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TYPE: PRT
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                                                                                                                                  Length 185;
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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MORATION:
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 52945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT APPLICATION NUMBER: US/09/747,377
PRIOR PILING DATE: 2000-12-22
PRIOR PLING DATE: 2000-10-22
PRIOR PLING DATE: 2000-10-3-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                             Query Match
9.8%; Score 94.5; DB 15;
Best Local Similarity 25.8%; Pred. No. 0.24;
Matches 47; Conservative 22; Mismatches 64;
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NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
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                                                               TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 48; Conserva
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US-10-087-192-984
                             SEQ ID NO 5
LENGTH: 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 CVPAECFDLLVRHCVACGLLRTPRPKPAGASSPAPRTALOPOESVGAGAGEAALPLPGLL
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                                                                      APPLICANT: Gross, Jane A.
APPLICANT: Xu, Wenfeng
APPLICANT: Two Wenfeng
APPLICANT: Henne, Randal M.
APPLICANT: Henne, Randal M.
TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor
FILE REPERENCE: 00-103
CURRENT APPLICATION NUMBER: US/10/008,063
CURRENT FILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO.
LENGTH: 184
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APPLICANT: Rixon, Mark W.
TITLE OF INVENTION: TACL-Immunoglobulin Fusion Proteins:
TITLE OF INVENTION: TACL-Immunoglobulin Fusion Proteins:
FILE REFERENCE: 01-20
CURRENT APPLICATION NUMBER: US/10/152,363A
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: 60/293,343
PRIOR FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 70
SEQ ID NOS: 70
SEQ ID NOS: 70
SEQ ID NOS: 70
SEQ ID NOS: 70
LENGTH: 184
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Sequence 2, Application US/10008063 Publication No. US20030092164A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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US-10-008-063-2
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Best Local Similarity
                                                   GENERAL INFORMATION:
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US-10-152-363A-60
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128 --- DKVII---LSPGISDATAPAWPPPGEDPGTTPP---- GHSVPVPATELGSTELVTTK 177
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Sequence 7, Application US/10380703

Publication No. US20040072188A1

SEMBRAL INFORMATION:

APPLICANT: Biogen, Inc.

APPLICANT: Thompson, Jeffrey S

APPLICANT: Thompson, Jeffrey S

FILE REFERENCE: BIOGG -0086

CURRENT AMBLOSE, Christine M

TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides

FILE REFERENCE: BIOGG -0086

CURRENT APPLICATION NUMBER: US/10/380,703

CURRENT FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-21

PRIOR PLING DATE: 2000-09-21

PRIOR PLING DATE: 2001-02-13

PRIOR PLING DATE: 2001-02-13

PRIOR PILING DATE: 2001-02-13

PRIOR PILING DATE: 2001-02-13

PRIOR PILING DATE: 2001-08-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PATENTIN version 3.1

SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.6%; Score 93; DB 17; Length 18. Best Local Similarity 26.5%; Pred. No. 0.33; Matches 48; Conservative 20; Mismatches 65; Indels
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                       US/10/742,634
                                                               PRIOR APPLICATION NUMBER: US 60/435,262
PRIOR FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 60/467,198
PRIOR FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
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Matches 48; Conservative
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US-10-380-703-7
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APPLICANT: Hilbert, David
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: Neutrokine-alpha Conjugate, Neutrokine-alpha Complex, and Uses Th
                                                                                                                                 128 ---DKVII---LSPGISDATAPAMPPPGEDPGTTPP----GHSVPVPATELGSTELVTTK 177
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                             8 CSQNEYFDSLLHACIPCQL-----RCSSNTP--PLTCQRYCNASVTNSVKGTNAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Biogen, Inc.
APPLICANT: Thompson, Jeffrey S
APPLICANT: Thompson, Jeffrey S
APPLICANT: Thompson, Jeffrey S
APPLICANT: Ambrose, Christine M
TITLE OF INVENTION: Receptor Nucleic Acids and Polypeptides
FILE REPERENCE: BIOG-0086
CURRENT APPLICATION NUMBER: US/10/380,703
CURRENT APPLICATION NUMBER: 60/233,152
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-02-13
PRIOR FILING DATE: 2001-08-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
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86.5%; Pred. No. 0.33;
1ve 20; Mismatches
  W---TCLGLSLIISLAVFVLMF---
                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/10380703 Publication No. US20040072188A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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161 FGAPALLGLALVLALVLVGLVSWRRRQRRLRGASSAEAPDGDKDAPRPL----- 209
                                                      108 RIGDEIILPRGLEYTVEECTC-----BDCIKSKPKVDSDHCFPLPAMEEGATILVTTK 160
                                                                            210 ---DKVII---LSPGISDATAPAWPPPGEDPGTTPP----GHSVPVPATELGSTELVTTK 259
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Publication No. US20030099990A1
Publication No. US20030099990A1
Publication No. US20030099990A1
APPLICANT: HYPORMATION:
APPLICANT: HALL-1 Receptor Molecules and Uses Thereof TILE REFERENCE: 01-1160-A
CURRENT APPLICATION NUMBER: US/10/251,947
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 7
LENGTH: 171
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TITLE OF INVENTION: TALL-1 Receptor Molecules and Uses Thereof
FILE REFRENCE: 01-1160-A
CURRENT APPLICATION NUMBER: US/10/251,947
CURRENT FILING DATE: 2002-09-20
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-251-947-7
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                                                                                                                                                                                                                         ; Search time 7.48624 Seconds (without alignments) 436.984 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Perfect score:
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Maximum DB
                                                                                                                                                                    protein
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No.
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ALIGNMENTS

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Rigao, Z.; Garbers, D.L.
7. Biol. Chem. 273, 3412-3421, 1998
A;Title: Species diversity in the structure of zonadhesin, a sperm-specific membrane prot
A;Reference number: Z22080; MUID:98123114; PMID:9452463
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5376 <GAO>
A;Cross-references: UNIPROT:088799; EMBL:U97068; NID:g3327420; PID:g3327421; PIDN:AAC2668
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1101 <GEI
A;Kesidues: 1-1101 <GEI
A;Cess-references: UNIPROT: 022378; EMBL: U39644; NID: g1049339; PID: g1049343; PIDN: AAA803
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:TIOE10.4
A;Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T10E10.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16840
Alternate names: sperm-specific membrane protein
,Species: Mus musculus (house mouse)
,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
,Accession: T42215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 32.1%; Score 64.5; DB 2; Length 5376; Best Local Similarity 35.1%; Pred. No. 16; Matches 13; Conservative 5; Mismatches 16; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Function:
A;Description: functions in multiple cell adhesion processes
A;Description: functions on the apical region of the sperm head
C;Keywords: cell adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1101;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CSONEYFDSLLHACIP-COLRCSSNTP--PLTCORYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 30.3%; Score 61; DB 2; Local Similarity 37.5%; Pred. No. 11; hes 12; Conservative 7; Mismatches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | | | | : | : | : | : | : | CSQSTVFNSDLNVCVPLAIQNSCDSSTQQPVC 382
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                                                           N;Alternate names:
                  zonadhesin - mouse
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A; Residues: 1-184 <LAA>
A; Residues: 1-184 <LAA>
A; Residues: 1-184 <LAA>
A; Residues: 1-184 <LAA>
A; Residues: 1-184 <LAA>
A; Residues: 1-184 <LAA>
A; Cross-references: UNIPROT: Q0223; EMBL: Z29574; NID: g471244; PIDN: CAA82690.1; PID: g4712
R; Laabi, Y: Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, EMBO J. 11, 3897-3904, 1992
A; Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;1 A; Accession: S31208
A; Accession: S31208
A; Accession: S31208
A; Residues: 1-184 <LAA2>
A; Residues: 1-184 <LAA2>
A; Cross-references: EMBL: Z14954; NID: g29407; PIDN: CAA78679.1; PID: g29408
A; Residues: 4-184 <LAA3>
A; Residues: 4-184 <LAA3>
A; Cross-references: EMBL: Z14955
C; Genetics: C; Genetics: CDB: EMBL: Z14955
C; Genetics: C; Construction CDB: EMBL: Z14955
C; Construction CDB: EMBL: Z14955
C; Construction CDB: EMBL: Z14955
C; Construction CDB: EMBL: Z14955
C; Construction CDB: EMBL: Z14955
C; Construction CDB: EMBL: Z14955
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C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
R;Nakagawa, T: Murakami, K.; Nakayama, K.
FEBS Lett. 327, 165-171, 1993
A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a A;Title: Identification of an isoform with an extremely large Cys-rich region of PC6, a A;Title: Identification of PC6, a A;Title: Identification of A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Identification of PC6, a A;Title: Iden
                                                                                                             B-cell maturation factor - human
B.cell maturation factor - human
B.scell maturation factor - human
B.Alternate names: BCM protein; BCMA protein; BEL protein
C;Species: Homo sapiens
C;Species: An-1995 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
C;Date: 27-Jan-1995 #sequence revision 27-Jan-1995 #text_change 09-Jul-2004
C;Accession: S4486; S31208; S3661
B.A.Flachi, Y.; Grass, M.P.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, A.
Nucleic Acids Res. 22, 1147-1154, 1994
A;Title: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire
A;Tetles: The BCMA gene, preferentially expressed during B lymphoid maturation, is bidire
A;Accession: 843486
A;Status: preliminary
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C;Species: Mus musculus (house mouse)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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Best Local Similarity 37.8%; Pred. No. 2.4;
Matches 14; Conservative 4; Mismatches 14; Indels 5.
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Pred. No. 3.2e-17
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Local Similarity 100.0%; Pred. No. 3.2
tes 34; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 16p13.1-16p13.1
A;Introns: 44/1; 93/1
C;Superfamily: human B-cell maturation factor
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R;Roebroek, A.J.; Creemers, J.W.; Pauli, I.G.; Kurzik-Dumke, U.; Rentrop, M.; Gateff, E. J. Biol. Chem. 267, 17208-17215, 1992
A;Title: Cloning and functional expression of Dfurin2, a subtilisin-like proprotein proc A;Reference number: A43434; MUID:92381036; PMID:1512259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1.1717 <SHO>
;Cross-references: UNIPROT:Q26566; EMBL:M86396; NID:g160957; PIDN:AAA29866.1; PID:g1609
;Note: sequence extracted from NCBI backbone (NCBIP:111129)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: fluke epidermal growth factor receptor homolog 1; protein kinase homology C;Keywords: alternative splicing; ATP; autophosphorylation; glycoprotein; phosphoprotein F;1-19/Domain: signal sequence #status predicted <81G>
F;20-171/Product: epidermal growth factor receptor homolog 1 #status predicted <MAT>
F;1018-1333/Domain: protein kinase homology KIN>
F;1026-1034/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor receptor homolog precursor - fluke (Schistosoma mansoni)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T34022
zonadhesin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
                                                                       C;Species: Drosophila melanogaster
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-1680 <ROE>
A;Cross-references: UNIPROT:P30432; GB:M94375; NID:g157461; PID:g157462
A;Note: sequence extracted from NCBI backbone (NCBIN:111933, NCBIP:111934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                    furin (EC 3.4.21.75) 2 - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Keywords: hydrolase; serine proteinase; transmembrane pro
F;409-652/Domain: subtilisin homology <SBT>
F;418,457,638/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSESEFYSOVEGOCRPCHASCGSCNGPADTSCTSC 1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 57; DB 1;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contains: protein-tyrosine kinase (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57.5; DB
Pred. No. 41;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: FlyBase: FBgn0004598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRCS 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                        Status: preliminary
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                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: FlyBase: Fur2
                                                                                                                              Accession: A43434
                                                                                                                                                                                                                                                                  Accession: A43434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A45558
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAIternate names: paired basic amino acid cleaving enzyme; proprotein convertase; serin (Species: Spodoptera frugiperda (fall armyworm)
(Species: Spodoptera frugiperda (fall armyworm)
(Spacession: T43251
R;Cieplik, M.; Klenk, H.
R;Cieplik, M.; Klenk, H.
R;Cieplik, M.; Klenk, H.
A;Description: Cloning and functional characterization of FURIN from Spodoptera frugiper A;Reference number: Z22368
  A,Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-758 <LAT>
A;Cross-references: UNIPROT:09GXR5; EMBL:U39851; NID:g1055062; PID:g1055068; PIDN:AAA810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1299 «CIE»
A;Cross-references: UNIPROT:Q26489; EMBL:Z68888; NID:g1167859; PID:e219690; PIDN:CAA9311
A;Experimental source: clone Sfurin 6; ovary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: responsible for the endoproteolytic processing of proproteins with specif
C; Keywords: hydrolase; serine proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiBabin, D.R.; Peanasky, R.J.; Goos, S.M.
Arch. Blochem. Blophys. 232, 143-161, 1984
A;Title: The isoinhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the prima
A;Reference number: 807127; MUID:84255715; PMID:6564898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chymotrypsin/elastase inhibitor - common roundworm
C;Species: Ascaris lumbricoides (common roundworm)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                              A;Gene: CESP:C23G10.8
A;Introns: 47/3; 237/3; 293/2; 405/3; 487/1; 577/3; 694/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C23G10.8
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Pred. No. 29;
5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 63;
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                                                                                                                                                                                                                                                                                        6; Indels
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                                                                                                                                                                                                                                 Score 59; DB 2;
Pred. No. 14;
6; Mismatches
preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: T43251
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                             8 DSLLHACIPCOLRCSSNTPPL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  furin (EC 3.4.21.75) - fall armyworm
                                                                                                                                                                                                                                       Query Match 29.4%;
Best Local Similarity 42.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 28.9%;
Local Similarity 37.1%;
hes 13; Conservative
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A; Residues: 1-63 <BAB>
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nes 13; Conserv
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Best Local S:
Matches 13,
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A,Map position: 5
A,Introns: 16/3
C,Superfamily: gliadin
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A;Experimental source: clone T23F1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T01519
R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; Gott
                                                                                            ext
                                                                                                                                                                                                             A,Residues: 1-2476 «HAR»
A,Cross-references: UNIPROT:Q28983; EMBL:U40024; NID:g1066465; PID:g1066466; PIDN:AAC484
A,Experimental source: strain Meishan; testis
C;Accession: T34022
R;Hardy, D.M.; Garbers, D.L.
J. Biol. Chem. 270, 26025-26028, 1995
A;Title: A sperm membrane protein that binds in a species-specific manner to the egg A;Title: A sperm membrane protein that binds in a species-specific manner to the egg A;Accession: T34022
A;Accession: T34022
A;Accession: T3402
A;Molecule type: mRNA
A;Molecule: Lype: mRNA
A;Residues: 1-2476 <HAR>
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A,Cross-references: UNIPROT:Q9ZUO0; EMBL:AF001308; NID:g2104523; PID:g3912931
A,Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T10M13.17.1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 09-Jul-2004
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hypothetical protein T23F1.6 - Caenorhabditis elegans
hypothetical protein T23F1.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25169
E;Wilkinson, J.
Submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: Zan
C;Function: may be involved in sperm adhesion to the zona pellucida
A;Description: may be involved in sperm adhesion to the zona pellucida
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submitted to the EMBL Data Library, May 1997
A;Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 989;
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 2; Length 2476;
Pred. No. 87;
8; Mismatches 14; Indels
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A;Accession: T25169
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Pred. No. 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.9%;
Best Local Similarity 31.6%;
Matches 12; Conservative
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nes 13, Conservative
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A; Accession: T01519
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A;Gene: CESP:T23F1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: T10M13.17.1
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A, Introns: 31/3
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A;Residues: 1-1513 <WIL>
A;Cross-references: UNIPROT:017970; EMBL:281573; PIDN:CAB04625.1; GSPDB:GN00020; CESP:MO: A;Experimental source: clone M02G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
E;Legan, P.K.; Rau, A.; Keene, J.N.; Richardson, G.P.
J. Blol. Chem. 272, 8791-8801, 1997
A;Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to comp. A;Reference number: 220771; MUID:97236843; PMID:9079715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Molecule type: mRNA

A,Residues: 1-2155 <LEGS.

A,Eresidues: 1-2155 <LEGS.

A,Experimental source: strain CD1; whole cochleae

A,Experimental source: strain CD1; whole cochleae

A,Note: non-collagenous protein only expressed in the inner ear, by cells both in and su
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                                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23681
R;Matthews, L.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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A;Introns: 23/3; 71/3; 121/3; 183/1; 1083/3; 1141/3; 1408/1; 1449/1
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DB 2; Length 330;
21;
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                                                       15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1372 CPPNSHYESCVSVCOP---RCAAIRLKSDCNHYC 1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1996 A; Reference number: 219781
  Score 55; DB 2
Pred. No. 21;
7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

27.4%; Score 55; DB
Best Local Similarity 44.8%; Pred. No. 76;
Matches 13; Conservative 3; Mismatches
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myosin heavy chain - rat
C;Species: Rattus norvegicus (Norway rat)
Query Match 27.4%;
Best Local Similarity 28.6%;
Matches 12; Conservative
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C;Accession: S46625; S56993
R;Purnelle, B.; Coster, F.; Goffeau, A.
Yeast 10, 1235-1249, 1994
A;Title: The sequence of a 36 kb segment on the left arm of yeast chromosome X identifie. ase gene ACO1 and two homologues to chromosome III genes.
A;Reference number: S46621; MUID:95274326; PMID:7754713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-758 <PUW>
A;Cross.references: EMBb:Z49481; NID:g1015584; PIDN:CAA89502.1; PID:g1015585; MIPS:YJL20
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A;Residues: 1-1574 <NAK>
A;Cross-references: UNIPROT:088281; EMBL:AB011532; NID:g3449293; PIDN:BAA32462.1; PID:g3
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: UNIPROT:P39529; EMBL:X77688; NID:g1183992; PIDN:CAA54752.1; PID:g547;
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R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
Romonics S1, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like motifs
A;Reference number: 214126; MUID:98360089; PMID:9693030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transmembrane protein; zinc
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  966 csagapcdavrgsci-cpagrwgprcagscppLrgLncsgic 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 10L
C;Superfamily: GAL4 zinc binuclear cluster homology
C;Reywords: DNA binding; nucleus; transcription regulation;
F;42-78/Domain: GAL4 zinc binuclear cluster homology <GAL4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R.Purnelle, B.; Coster, F.; Goffeau, A.
submitted to the Protein Sequence Database, September 1995
A.Reference number: S56977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
26.6%; Score 53.5; D
Best Local Similarity 50.0%; Pred. No. 64;
Matches 11; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-758 <PUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: S56993
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A;Gene: MEGF6
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                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1980 «REI»
A;Cross-references: UNIPROT:Q63358; EMBL:X77609; NID:g639998; PIDN:CAA54700.1; PID:g6399
C;Superfamilly: rat myosin heavy chain; myosin motor domain homology; protein kinase C zi
C;Keywords: nucleotide binding; P-loop
F;149-942/Domain: myosin motor domain homology «MMOT»
F;139-246/Region: nucleotide-binding motif A (P-loop)
F;1593-1641/Domain: protein kinase C zinc-binding repeat homology «KZN»
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AS9256

Woosin-IXD [similarity] - human
G;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 10-May-2056; 10-May-2004
D;Date: 10-May-2056; MulD: 10-May-2004
D;Date: 10-May-2056; MulD: 10-May-2004
D;Date: 10-May-2056; MulD: 10-May-2004
D;Date: 10-May-2056; MulD: 10-May-2004
D;Date: 10-May-2060
D;Date: 10-May-2004
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A,Residues: 1-2022 < WIR>

A,Kesidues: 1-2022 < WIR>

A,Cross-references: UNIPROT: 014788; GB:U42391; NID:g1147782; PIDN:AAC50402.1; PID:g11477

R,Bement, W.M.; Hasson, T.; Wirth, J.A.; Cheney, R.E.; Mooseker, M.S.

Proc. Natl. Acad. Sci. US.A. 91, 6549-6553, 1994

A,Title: Identification and overlapping expression of multiple unconventional myosin gen

A,Reference number: A55758; MUID:94294418; PMID:8022818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                C; Accession: S54307

R; Reinhard, J.; Scheel, A.A.; Diekmann, D.; Hall, A.; Ruppert, C.; Baehler, M. EMBO J. 14, 697-704, 1995

A; Title: A novel type of myosin implicated in signalling by rho family GTPases. A; Reference number: S54307; MUID: 95188874; PMID: 7882973

A; Recession: S54307

A; Ratus: preliminary; nucleic acid sequence not shown
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        15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
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N;Alternate names: probable membrane protein VJL206c; protein J0316
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 26.9%; Score 54; DB 2; Length 1980; Best Local Similarity 52.9%; Pred. No. 1.3e+02; Matches 9; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2022;
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Pred. No. 1.3e+02;
2; Mismatches 6;
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A;Molecule type: mRNA
A;Residues: 234-322 <RES>
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PCLLRCPDNSDPLTSMK 1868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 PCQLRCSSNTPPLTCQR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCQLRCSSNTPPLTCQR 32
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ilarity 52.9%;
Conservative
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A;Gene: GDB:MYO9B; OMIM:602129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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Length 255,

DB 2; 39;

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A.Gross-references: UNIPROT:09XUSO; EMBL:Z81573; PIDN:CAB04626.1; GSPDB:GN00020; CESP:MO.A.Experimental source: clone M02G9
                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein M02G9.3 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                    20 CSMDSFFDELLRDSHACTHTHTCTPPGPENTHTHTC 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rimatthews, L. submitted to the EMBL Data Library, November 1996 A; Reference number: 219781 A; Accession: T23682 A; Accession: T23682 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
                                                                                                                                                                                                                                   1 CSONEYFDSIL---HACI---PCQLRCSSNTPPLTC
                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 25.9%; Score 52; Best Local Similarity 35.3%; Pred. No. 4 Matches 12; Conservative 3; Mismatch
                                                                                                                              Score 52;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:M02G9.3
A;Map position: 2
A;Introns: 20/3; 76/2; 182/3; 223/3
                                                                                                                              25.9%;
38.9%;
                                                                                                                           Query Match 25.9
Best Local Similarity 38.9
Matches 14; Conservative
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Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-547 <NHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: T23682
                     C;Genetics:
A;Gene: At2g16770
A;Map position: 2
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A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein At2g16770 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: A84544
R;Lin, X.; Raul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Busus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                                     A;Map position: 1
A;Introns: 87/1; 98/1; 126/2; 201/3; 343/3; 406/1; 576/3; 656/1; 825/3; 869/1; 909/1; 96
A;Introns: 87/1; 1850/1; 1850/3; 1896/1; 2003/3; 2035/3; 2082/3; 2119/1; 2144/1; 2200/2; 227
F;243-279/Pomain: LDL receptor ligand-binding repeat homology <LDL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:012307; EMBL:Z67750; NID:91061256; PIDN:CAA91584.1; PID:9106
A;Residues: 1-2824 WIL>
A;Crose-references: UNIPROT:P90891; EMBL:Z81091; PIDN:CAB03143.1; GSPDB:GN00019; CESP:F9
A;Experimental source: clone F55H12
C;Genetics:
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Nylternate names: hypothetical protein D1510
C;Species: Saccharomyces crevitain D1510
C;Accession: Sel051; S67714
R;Pohl, T.M.
submitted to the BMBL Data Library, November 1995
A;Reference number: S61010
A;Accession: S61051
A;Molecule run.
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                                                                                                                                                                                                                                                                                                                26.4%; Score 53; DB 2; Length 2824; 36.1%; Pred. No. 2.2e+02; tive 7; Mismatches 14; Indels
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C;Superfamily: Saccharomyces hypothetical protein YDL162c
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2574 CEQGIFQNVSNSDSCIPCSDLSENAISIPVICQSIC 2609
                                                                                                                                                                                                                                                                                                                                                                                                                           1 CSQNEYFD-SLLHACIPC-QLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: $67708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ::| | | : | : | CNRNSYCSRWFYCCLTLSSFCSLRC---VPPL 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 52.5; DB
Pred. No. 18;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSQNEYFDSLLHACIP----CQLRCSSNTPPL 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 26.1%;
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: SGD:S0002321
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Best Local Similarity 36.1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-118 < POW>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-255 <STO>
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A; Residues: 1-118 < POH>
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S61051
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A84544
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DB 2; Length 294;

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A;Gene: CESP:K03Al.3
A;Introns: 33/3; 50/2; 95/1; 118/3; 181/2; 293/3; 342/1; 371/3; 390/2; 451/1; 484/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
5
                                                                                                                                                                                                                                                                        Cigpecies: Caenorhabditis elegans
CiDate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
CiAccession: T34318
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cross-references: EMBL:U41625; PIDN:AAA83324.1; CESP:K03A1.3
                                                                                                                                                                                                                                                                                                                                                                      submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid K03A1
A;Reference number: Z21505
                                                                                                                                                                                                                                            Nypothetical protein K03A1.3 - Caenorhabditis elegans
                                                                                   SSNSY-----CIPVCMAQCQSSCTTPICQQQC 73
                                                    2 SQNEYFDSLLHACIP-CQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
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D88550
protein ZC84.6 [imported] - Caenorhabditis elegans
  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCOLR 20
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A;Accession: S57816
A;Status: preliminary
A;Accession: breliminary
A;Accession: preliminary
A;Accession: preliminary
A;Accession: 1-63 access
A;Cross-references: UNIPROT:P25404; EMBL:U15539; NID:g558864; PIDN:AAA80485.1; PID:g5588
B;Cammue, B.P.; De Bolle, M.F.; Terras, F.R.; Proost, P.; Van Damme, J.; Rees, S.B.; Van
J; Biol. Chem. 267, 2228-2233, 1992
A;Title: Isolation and characterization of a novel class of plant antimicrobial peptides
A;Reference number: A42316; MUID:9212929; PMID:1733929
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A;Cross-references: UNIPROT:Q06985; EMBL:Z19580; NID:g297801; PIDN:CAA79631.1; PID:g2978:
C;Superfamily: Drosophila developmental protein sina; RING finger homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P61092; EMBL:Z19579; NID:g297034; PIDN:CAA79630.1; PID:g2970 C;Superfamily: Drosophila developmental protein sina; RING finger homology
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(Species: Mus musculus (house mouse)
C;bace: 13-3na-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 148764; 835754
C;Accession: 148764; Senior, P. V.; Bowtell, D.D.
Development 117, 1333-1343, 1993
A;Title: Isolation and characterisation of murine homologues of the Drosophila seven in A;Reference number: 148763; MUID:94008536; PMID:8404535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Della, N.G.; Senior, P.V.; Bowtell, D.D. Development 117, 1333-1343, 1993
A;Title: Isolation and characterisation of murine homologues of the Drosophila seven in A;Reference number: I48763; MUID:94008536; PMID:8404535
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 148763; S35753
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Note: sequence extracted from NCBI backbone (NCBIP:78217)
               A; Reference number: S57815; MUID:95375234; PMID:7647302
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A;Molecule type: mRNA
A;Residues: 1-282 <RES>
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; Pred. No. 14;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 FDSLLHACIPCQ --- LRCSSNTPPLTCQRYC 34
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41.9%; Pred. No. 48;
tive 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LLHACIPCOLRCSSNT-PPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.6%;
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nes 13; Conservative
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Best Local Similarity 38.3.
Best Local 10; Conservative
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A.Molecule type: protein
A.Residues: 28-63 <CAM>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A42316
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: D88550
B;Ancession: D88550
B;Anconymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nemacode C. elegans: a platform for investigating biolog A;Neference number: A7500; MUID:99069613; PMID:9851916
A;Note: see websites genome wustl.edu/gsc/C elegans/ and www sanger.ac.uk/Projects/C ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Noteus: preliminary
A;Noteus: 1-1474 <STO>
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F;220-274/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;343-395/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;44-492/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;44-698/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;546-598/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;546-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;554-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPII>F;654-706/Domain: animal Kunitz-type proteinase inhibitor homology <BPII
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A;Gene: ZC84.6
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C;Species: Caenorhabditis elegans
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S28291
R;Thomas, K.
Birhomas, K.
A;Reference number: S28285
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-2844 <THO>
A;Cross-references: UNIPROT:Q03610; EMBL:Z19157
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Matches 12; Conservative
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;Residues: 1-927 <WIL>
;Cross-references: UNIPROT:002364; EMBL:Z81527; PIDN:CAB04279.1; GSPDB:GN00023; CESP:T03.
;Experimental source: clone F35E12
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A;Experimental source: clone C1481
R;Kershaw, J.
Submitted to the EMBL Data Library, June 1994
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A;Cross-references: EMBL:234799; PIDN:CAA84320.1; GSPDB:GN00021; CESP:F34D10.2
A;Experimental source: clone F34D10
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A;Molecule type: DNA
A;Residues: 1-927 <WIZ-A;AL;ASSIGNES: 1-927 <WIZ-A;ASSIGNES: 1-927 <WIZ-A;A;Cross-references: EMBL:281110; PIDN:CAB03262.1; GSPDB:GN00023; CESP:T01D3.6
A;Experimental source: clone T01D3
      hypothetical protein T01D3.6 - Caenorhabditis elegans
Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21772; T24296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F34D10.2 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C.Accession: T19275; T21723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 5
A;Introns: 38/2; 87/3; 128/2; 242/2; 374/3; 416/3; 734/3; 842/3; 857/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.5; DB 2; Length 927;
Pred. No. 1.3e+02;
3; Mismatches 19; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468 CTEFTYFLQYCQLALPQVAMNQNWRAQINCPLACPLNAHPSTCTSSC 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.6%; Score 51.5; DB 2; Length 999; Best Local Similarity 48.3%; Pred. No. 1.4e+02; Matches 14; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---CQLRCSSNTPPLTCQRYC
                                                                                                                                                                                                                A;Accession: T21772
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T21723
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                  R;Steward, C.
submitted to the EMBL Data Library, November 1996
A;Reference number: 219470
                                                                                                                                                                                                                                                                                                                                                                                                                    R;Sreward, C.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19870
A;Accession: T24296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 YFDSLLHACIPCQL-RCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.6%;
Best Local Similarity 25.5%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSONEYFDSLLHACIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: Z19464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-999 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: CESP: F34D10.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Gene: CESP: T01D3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C, Genetics
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                                                                                                                                                                            hypothetical protein ZK287.1 - Caenorhabditis elegans
C;Species: Genorhabditis elegans
C;Species: Genorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27827
R;McMurray, A.
Bubmitted to the EMBL Data Library, April 1996
A;Reference number: Z20425
A;Accession: T27837
A;Accession: T27837
A;Accession: T27837
A;Accession: T27837
A;Accession: Z27837
A;Residues: 1-497 <WIL>
A;McDecule type: DNA
A;Residues: 1-497 <WIL>
A;Cross-references: UNIPROT:Q23460; EMBL:Z70757; PIDN:CAA94805.1; GSPDB:GN00023; CESP:ZR
A;Experimental source: clone ZK287
A;Gene: CESP:ZX287.1
A;Map position: 5
A;Introns: 20/1; 44/2; 99/3; 339/3; 443/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-915 <WIL>
A;Cross-references: UNIPROT:002364; EMBL:281527; PIDN:CAB04280.1; GSPDB:GN00023; CESP:TC
A;Experimental source: clone F35E12
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A;Experimental source: clone T01D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein T01D3.6b - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cispecies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Cispecies: T1773, T24297
Risterence number: 219470
A;Reference number: 219470
A;Reference number: 219470
A;Accession: T21773
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Gene: CESP:T01D3.6b
A;Map position: 5
A;Introns: 38/2; 87/3; 128/2; 374/3; 404/3; 722/3; 830/3; 845/1
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A;Reference number: Z19870
A;Accession: T2423-A;Accession: T2423-A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-915 <WIZ>
Query Match
25.6%; Score 51.5; I
Best Local Similarity 38.5%; Pred. No. 78;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15 CVASQGRCSADTCPCVAARKTCDEHC 40
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RESULT 31 T21772

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A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C., Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luxos, J.S.; Malti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A; Authors: Salzberg, S.L.; Chwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A; Title: Sequence and analysis of chromsome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:121016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L., euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Niture 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUD:20083487; PMID:10617197
A; Status: preliminary
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-746 <STO>
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Rivillary A.; Therry, A.; Dahlback, B.

J. Immunol. 153, 4190-4199, 1994

A;Title: Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains prov A;Reference number: 146001; MUID:95015909; PMID:7930621

A;Accession: 146001

A;Accession: 146001

A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-610 <HIL>
A; Cross-references: UNIPROT: Q28065; EMBL: Z31693; NID: g469117; PIDN: CAA83498.1; PID: g46911
G; Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
F; 50-107/Domain: complement factor H repeat homology <FH1>
F; 112-169/Domain: complement factor H repeat homology <FH2>
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: UNIPROT: Q9S9J8; GB: AE005173; NID: 94646199; PIDN: AAD26872.1; GSPDB: GN(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein At2g21840 [imported] - Arabidopsis thaliana (jobecies: Arabidopsis thaliana (mouse-ear cress) Arabidopsis thaliana (mouse-ear cress) (c).Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 (c).Accession: G84605
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C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C.Accession: 146001; S43190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.4%; Score 51; DB 2; Length 653
42.3%; Pred. No. 1.18+02;
ive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.4%; Score 51; DB 2; Length 746
28.6%; Pred. No. 1.3e+02;
ive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 FDEMFYHCSACNFTLDLRCVSLPPPL 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4b-binding protein alpha chain - bovine
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Best Local Similarity 28.6
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                              A;Accession: G96675
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A,Map position: 1
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A;Map position: 2
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A;Residues: 1-2120 <COU>
A;Cross-references: UNIPROT:Q9YH85; EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAAG
A;Note: non-collagenous protein only expressed in the inner ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable transcription factor F12K22.14 [imported] - Arabidopsis thaliana Grobable transcription factor F12K22.14 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: E96612
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.Y.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, M.; Soney, T.; Rowley, D.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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A,Map position: 1
C,Superfamily: Arabidopsis thaliana probable transcription factor F12K22.14; RING finger
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996675
hypothetical protein T23K8.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: 696675
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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A,Residues: 1-641 <STO>
A,Cross-references: UNIPROT:09FVS3; GB:AE005173; NID:g11079528; PIDN:AAG29238.1; GSPDB:
                                                                                                    alpha tectorin - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 02-892-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T30243
R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.
Hear. Res. 130, 62-74. 1999
A;Title: Chick alpha tectorin: molecular cloning and expression during embryogenesis. A;Reference number: 220783; MUID:99251817; PMID:10320099
A;Recession: T30243
A;Status: preliminary; translated from GB/EMBL/DDBJ
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1345 CPPNSHYES----CVSLCQPRCAAIRLKSDCGHYC 1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CSONEYFDSLLHACIP-COLRCSSNTPPLTCORYC 34
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Best Local Similarity
Matches 11; Conserva
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hypothetical protein ORF23 - Lymantria dispar nuclear polyhedrosis virus
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMnPv
C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMnPv
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30370
R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohrn Virology 253, 17-34, 1999
A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria di)
A;Reference number: Z20836; MUID:99124785; PMID:9887315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C,Accession: C81272

R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling:
R;Parkhill, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000

A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hype:
A;Reference number: A81250; MUID:20150912; PMID:10688204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-376 < PAR>
A;Residues: 1-376 < PAR>
A;Cross-references: UNIPROT:Q9PNO5; GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73721
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NyAlternate names: P55 tumor necrosis factor receptor; TNF receptor type 1
NyContains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein
C;Speies: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004
C;Accession: A38208; A34899; A34800; A3655; C36555; A38281; S12057; JT0758; A60231; A38265; A38268; A38268; A38268; MID: 92250049; PMID: 1315717
A;Fitle: Structure of the human TNF receptor 1 (p60) gene (TNRF1) and localization to challe.
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A;Residues: 1-455 <PUC>
A;Cross-references: UNIRKOT:P19438; GB:M75864; GB:M75865; GB:M75866; NID:g339748; PIDN:AA
R;Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslaue
Cell 61, 351-359, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable aminotransferase (degT family) Cj1294 [imported] - Campylobacter jejuni (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 342;
86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: Cj1294
C;Superfamily: erythromycin resistance protein
                                                                                                                                                                                                                                                                                                                                                                                                                                           11arity 50.0%; Pred. No. 8 Conservative 1; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 ACIRCKSRFYKNNPILYCSR 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 ACIPCQLRCSSNTPPLTCQR 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
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s10332
ubiquitin / ribosomal protein CEPS2 - common tobacco (fragment)
N;Alternate names: ubiquitin fusion protein
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: S10332
Nucleic Acids Res. 18, 4007, 1990
A;Title: Sequence of a ubiquitin carboxyl extension protein of Nicotiana tabacum.
A;Reference number: S10332; MUID:90326543; PMID:2165257
A;Molecule type: DNA
A;Residues: 1-74 <GEN
A;Residues: 1-74 <GEN
A;Cross-references: UNIPROT:P19379; EMBL:X53011
C;Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; ubiq
C;Reywords: DNA binding; protein Dissynthesis; ribosome; zinc finger
F;1-2/Product: ubiquitin (fragment) #status predicted <UEP>F;3-74/Domain: ribosomal protein CEP52 #status predicted <RIB>F;2-61/Region: zinc finger CCCC motif
F;22-61/Region: zinc finger CCCC motif
F;68-74/Region: nuclear location signal
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                                                                                                                                                                                                Length 610;
                                                                                                                                                                                                                                                9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Indels
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                                                                                       <FH6>
                                                                                                                 <FHR>
                                                                                                                                          <FH8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :|| : | :|: | :|: | 38
4 CGKNEVWIE----CIGCELKCGQDENIPCALMCRPPSCE 38
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                                                                                                                                                                                                                                                                                                                               F;239-294/Domain: complement factor H repeat homology F;299-362/Domain: complement factor H repeat homology F;366-425/Domain: complement factor H repeat homology F;429-483/Domain: complement factor H repeat homology F;487-541/Domain: complement factor H repeat homology
                                                                                                                                                                                                                                                                                                   6 YFDSLLHAC-----IPCQLRCSSNTPPLTCQ 31
                                                                                                                                                                                        Query Match 25.1%; Score 50.5; DB 1; Best Local Similarity 32.4%; Pred. No. 1.2e+02; Matches 12; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50; DB 2; Pred. No. 21; 6; Mismatches
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  complement factor H
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Best Local Similarity 30.8%;
Matches 12; Conservative
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Best Local Similarity 44.4%;
F;174-234/Domain:
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Wed Feb

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A;Cross-references: GDB:125913; OMIM:191190
A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 128/1; 184/2; 209/1; 247/1; 256/3; 353/1
A;Introns: 13/3; 65/1; 108/1; 128/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor; transmembrane protein
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>F;2-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>F;30-211/Domain: extracellular #status predicted <ATS-F;44-82/Domain: NGF receptor repeat homology <NG1>F;44-82/Domain: NGF receptor repeat homology <NG2>F;120/Product: Time to the top the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of the top of t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
                                                                                                                                                                                                                                                                                                                                                           A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence A;Reference number: A35010; MUID:90110215; PMID:2153136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Gosci. Botoechnol. Biochem. 58, 2266-2268, 1994
Title: Amino acid sequence of natural tunor necrosis factor alpha inhibitor purified
Reference number: JC2404; MUID:95128033; PMID:7765720
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27318
R;McMurray, A.
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F;235-455/Domain: intracellular #status predicted <INT>
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           521/3
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Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>
Experimental source: urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10,
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          A;Reference number: A60594; MUID:89171156; PMID:2924890 A;Accession: A60594
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A;Molecule type: DNA
A;Residues: 1-561 <WIL>
                                                                                                             A,Molecule type: protein
A,Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS.
A,Experimental source: renal failure patient urine
R,Engelmann, H, Novick, D.; Wallach, D.
J. Biol. Chem. 265, 1531-1536, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: protein
Residues: 41-45 <ENG>
Experimental source: normal urine
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A;Accession: T27318
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Matches 12; Conserv
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Best Local Similarity
Matches 12; Conserv
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Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recep. Reference number: A34899; MUID:90235284; PMID:2158862; A34899
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A; Residues: 1-455 <GRA>
A; Cross-references: GB M37764
A; Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372
R; Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann
EMBO J. 9, 3269-3278, 1990
A; Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ
          A;Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recept A;Reference number: A34899; MUID:90235284; PMID:2158862
A;Reference number: A34899
A;Molecule type: mRNA
A;Residues: 1-455 <-LOE>
A;Residues: 1-455 <-LOE>
A;Residues: 1-455 <-LOE>
A;Residues: 1-455 <-LOE>
A;Residues: 1-455 <-LOE>
A;Residues: 1-455 <-LOE>
A;Residues: 1-455 <-LOE>
A;Residues: 1-451 <-LOE
A;Residues: 1-451 <-LOE
A;Rote: part of this sequence, including the amino end of the mature protein, confirmed A;Rote: part of this sequence, including the amino end of the mature protein, confirmed A;Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.Cell 61, 361-370, 1990
A;Title: Molecular cloning and expression of a receptor for human tumor necrosis factor. A;Reference number: A34900; MUID:90235285; PMID:2158863
A;Accession: A34900.
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A, Molecule type: protein

A, Residues: 30-38141-53, XX, 55-79, XXX, 82-94, NKY; XXX, 100-104,107-128,162-167, XX, 169-2

A, Note: the purified protein, called tumor necrosis factor binding protein, is a soluble 
R, Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.

Proc., Natl. Acad. Sci. US.A. 87, 7380-7384, 1990

A, Title: Cloning of human theorosis factor (TNF) receptor CDNA and expression of re

A, Reference number: A38281; MUID:91017509; PMID:2170974
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A:Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
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A;Retenaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor (soluble tumor necrosis facto
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K;Seckinger, P.; Vey, B.; Turcatti, G.; Wingfield, P.; Dayer, J.M.
Eur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequend
A;Reference number: A60231; MUID:90292116; PMID:2113477
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A;Residues: 41-60 cGAT>
A;Reparimental source: cancer patient serum
R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, C.; Thysell, H.; Grubb, A.; Adolf, G.
Bur. J. Haematol. 42, 270-275, 1989
A;Title: Isolation and characterization of a tumor necrosis factor binding protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1455 <SCH>
A; Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745
A; Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745
A; Cross-references: GB:M3294; NID:G10804; M.; Scheurich, P.; Pfizenmaler, K.; Lantz, M.; DNA, Cell Biol. 9, 705-715, 1990
A; Title: Molecular cloning and expression of human and rat tumor necrosis factor receptca A; Reference number: A36555; MUID:91090841; PMID:1702293
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A; Residues: 1-455 <NOP>
A; Rosidues: 1-455 <NOP>
A; Notes references: EMBL: X55313; NID: G37223; PIDN: CAA39021.1; PID: G37224
A; Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends,
R; Kemper, O.; Wallach, D.
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A;Crose-references: GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:g339756
A;Accession: C36555
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A.Reference number: $12057; MUID:91006021; PMID:1698610
A.Accession: $12057
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A;Accession: A38258
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A; Residues: 1-455 <SCF
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Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.,
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II
A;Authors: Salzberg, S.E.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, II
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:Q9ZVU3; GB:AE005173; NID:g4204269; PIDN:AAD10650.1; GSPDB:GNU
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A;Reference number: A82950; MUID:20437337; PMID:10984043
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C;Genetics:
A;Gene: CESP:Y68A4A.10
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A;Molecule type: DNA
A;Residues: 1-392 <WIL>
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Best Local Similarity
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A;Residues: 1-1360 <STO>
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A;Molecule type: DNA
A;Residues: 1-216 <STO>
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A, Map position: 1
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R;McMurray, A.
Richardato the EMBL Data Library, August 1997
A;Reference number: Z20343
A;Accession: T27319
A;Accession: T27319
A;Accession: T27319
A;Reference number: Z20343
A;Recession: T27319
A;Residues: DNA
A;Residues: 1-626 <WIL>
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Simcusza... 1993;
Submitted to the EMBL Data Library, June 1996
Submitted to the EMBL Data Library, June 1996
Simple to the EMBL Data Library, June 1996
A; Reference number: 219762
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-922 <WILL>
A; Construction: UNIPROT: 021418; EMBL: 275545; PIDN: CAA99886.1; GSPDB: GN00019; CESP: XI
A; Experimental source: clone K10D3
A; Experimental source: clone K10D3
A; Constructs: CSP: X10D3.4
A; Map position: 1
A; Map position: 1
A; Introns: 60/1; 228/1; 355/1; 743/1; 802/1; 885/2
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hypothetical protein T5A14.15 [imported] - Arabidopsis thaliana

hypothetical protein T5A14.15 [imported] - Arabidopsis thaliana

(s) Species Naraloopsis thaliana (mouse-ear cress)

C) Species O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C) Accession: F96596

R) Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
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C;Species: Caenorhabditis elegans
C;Pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23573
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Best Local Similarity 32.4%; Pred. No. 1.4e+02;
Matches 12; Conservative 3; Mismatches 12; Indels
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                                                                                                                                   499 CRSNEKFE-----PCKTVCSDIKCNEEPRFCPQVC 528
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                                           CSQNEYFDSLLHACIPCQLRCSS---NTPPLTCQRYC 34
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Best Local S:
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RESULT 49
T30558
resistance protein RGC2J - garden lettuce
C;Species: Lactuca sativa (garden lettuce)
C;Species: Lactuca sativa (garden lettuce)
C;Decies: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: 130558
R;Meyers, B.C.; Chin, D.B.; Shen, K.A.; Sivaramakrishnan, S.; Lavelle, D.O.; Zhang, Z.; Plant Cell 10, 1817-1832, 1998
A;Title: The major resistance gene cluster in lettuce is highly duplicated and spans sev A;Reference number: 220859; MUID:99030190; PMID:9811791
A;Accession: T30558
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1847 cMEY>
A;Residues: 1-1847 cMEY>
A;Cross-references: UNIPROT:Q92769; EMBL:AF072271; NID:g4139035; PID:g4139036; PIDN:AADG C;Genetics: 894/3; 1069/3; 1293/3; 1838/3
A;Note: RGC2J
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Cispecies: Neurospora crassa
Cibate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001
Cibate: 05-May-2000 #sequence_revision 05-May-2000 #text_change 16-Feb-2001
Cischulte up 1: Aign, V; Hoheisel, J; Brandt, P; Fartmann, B; Holland, R; Nyakatura,
submitted to the Protein Sequence Database, April 2000
A; Reference number: 224541
A; Accession: T48828
A; Accession: T48828
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-189 <SCH>
A; Cross-references: EMBL: AL353821; GSPDB: GN00112; NCSP: 68B2.120
A; Experimental source: cosmid contig 68B2; strain 74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 24.6%; Score 49.5; DB 2; Length 1847; Best Local Similarity 35.7%; Pred. No. 4.1e+02; Matches 10; Conservative 5; Mismatches 12; Indels 1.
                                                                                              Query Match 24.6%; Score 49.5; DB 2; Length 392; Best Local Similarity 40.9%; Pred. No. 1.18+02; Matches 9; Conservative 6; Mismatches 6; Indels 1
A;Map position: 5
A;Introns: 45/2; 74/3; 139/3; 175/2; 190/3; 241/3; 305/3; 356/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 24.4%; Score 49; DB 2; Length 189; Best Local Similarity 41.2%; Pred. No. 69; Matches 7; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: Neurospora crassa hypothetical protein 68B2.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein 68B2.120 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        567 YDKLMYPLLPSSLECSTNVRVLHL-HYC 593
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Job time : 9.48624 secs
                                                                                                                                                                                                                                                                              189 SCLPCQ-TCASFIDPMSEKATC 209
                                                                                                                                                                                                                                       13 ACIPCOLRCSSNTPPLTCORYC 34
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MEDLINE-94218255; PubMed-8165126;
Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;
"The BCMA gene, preferentially expressed during B lymphoid maturation,
is bidirectionally transcribed.";
Nucleic Acids Res. 22:1147-1154(1994).
                                                                                                                                                                                                                                                             Laabi Y., Gras M.P., Carbonnel F., Brouet J.C., Berger R.,
Larsen C.J., Tsapis A.;
"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene
by a t (4,16) (q26,p13) translocation in a malignant T cell lymphoma.";
EMBO J. 11:3897-3904(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99425270; PubMed=10493829; Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gs.washington.edu).",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S., Sherwood J.K., Sherwood A.M., Leithauser B.J., Nickerson D.A.; "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu)." Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TNF receptor family member BCMA (B cell maturation) associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND VARIANTS VAL-54; VAL-65; VAL-75; ASN-81 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21419161; PubMed=11528522; DOI=10.1038/sj/gene/6363770; Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.; Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis."; denes Immun. 2:276-279(2001).
                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20363816; PubMed=10903733;
Hatzoglou A., Roussel J., Bourgeade M.-F., Rogier E., Madry C.,
Inoue J.-I., Devergne O., Tsapis A.;
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                                                             01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
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Tumor necrosis factor receptor superfamily member 17 (B-cell
                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION. TISSUE=Lymph node, and Peripheral blood leukocytes; MEDLINE=93010984; PubMed=1396583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION, AND INTERACTIONS WITH TRAF1 AND TRAF3.
                                       184 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANT THR-153.
                                                                                                                     maturation protein).
Name=TNFRSF17; Synonyms=BCMA, BCM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 165:1322-1330(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomics 60:295-308 (1999).
                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                           Mammalia; Euther
NCBI_TaxID=9606;
                                    HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION
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                     FR17_HUMAN
        RESULT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on institute use by non-profit institutions as long as its content is in no ways modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"B cell maturation protein is a receptor for the tumor necrosis factor
family member TALL-1.";
Moore M., Littau A., Grossman A., Haugen H., Foley K., Blumberg H., Harrison K., Kindsvogel W., Clegg C.H.;
"TAGI and BCMA are receptors for a TNF homologue implicated in B-cell annulpi disease".
                                                                                                                                                                                                                MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802; Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stollna M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.; "APRIL and TALL-I and receptors BCMA and TACI: system for regulating humoral immunity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).

-!- FUNCTION: Receptor for TNRSF134/BLyS/BAFF and TNFSF13/APRIL.

Promotes B-cell survival and plays a roll in the regulation of humoral immunity. Activates NF-kappa-B and JNK.

-!- SUBGNIT: Associates with TRAFI, TRAF2, TRAF3, TRAF5 and TRAF6.

-!- SUBGNILUAR LOCATION: Type III membrane protein. Plasma membrane and perinuclear Golgi-like structures.

-!- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells or monocytes.
-!- DISEASE: Involved in a form of T-cell acute lymphoblastic leuk (T-ALL) by a chromosomal translocation t(4,16) (q26,p13) which involves TWRRSF1 and IL2.
-!- SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breakpoint for translocation to form IL2/TNFRSF17 oncogene.
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GO; GO:0005886; C:plasma membrane; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0008283; P:receptor activity; TAS.
GO; GO:0007275; P:development; TAS.
GO; GO:0007165; P:signal transduction; TAS.
3D-structure; Chromosomal translocation; Immune response;
Polymorphism; Proto-oncogene; Receptor; Signal-anchor; Transmembr DOMAIN
TRANSMEM 55 77 Signal-anchor for type III membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERACTIONS WITH TRAFS AND TRAFG.
MEDLINE=20381353; PubMed=10908663; DOI=10.1073/pnas.160213497;
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                                                                                                                                                                                         FUNCTION, AND INTERACTIONS WITH APRIL AND BAFF
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By similarity.
By similarity.
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EMBL; AYS09112; AAR84240.1; -.
PIR; 343486; 543486.
PDB; 10QD; X-ray; K/L/M/N/O/P/Q/R=8-46.
Genew; HGNC:11913; TNFRSF17.
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                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Immunol. 1:252-256(2000)
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EMBL; Z29574; CAA82690.1; -.
EMBL; U95742; AAB67251.1; -.
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                                                                                                                             Nature 404:995-999(2000).
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37
41
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                                                                                            autoimmune disease.
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MEDINE=2238825; PubMed=12477932;

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Klausher R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

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Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC058291; AAH58291.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                              /FTIG=VAR 018759.
277AF11E2767D932 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor necrosis factor receptor superfamily, member 17.
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                                                                                                                                                                                                                                                                                                                      100.0%; Score 201; DB 1; 100.0%; Pred. No. 1.6e-18;
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                           ? -> V.
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Matches 34; Conservative
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Best Local Similarity
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Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 17 (B-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 184;
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                                                                                                                                                                                                                                                                         Numor necrosis factor receptor superfamily, member 17.
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                                                                                                                                                                                                                                         Last annotation update)
                                                                                                                                                                                                Last sequence update)
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Pred. No. 1.6e-18;
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                                                                                184 AA
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SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
                                                                                                                                                            Created)
                                                                                PRT;
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Matches 34; Conservative
                                                                                PRELIMINARY;
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Name=Tnfrsf17; Synony
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STRAIN=C57BL/6J; TISSUB=Mammary gland;

MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,

A plachul R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A plachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B prophere M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,

R aha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A.,

R Hichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                Yasunishi A., Yoshino M., Waterston R., Iander E.S., Rogers J., Birney E., Hayashizaki Y.; Waterston R., Lander E.S., Rogers J., "Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length CDMAs.";
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-!- FUNCTION: Receptor for TNYSF138/BLy8/BAFF and TNYSF13/APRIL.
Promotes B-cell survival and plays a role in the regulation of humoral immunity. Activates NF-kappa-B and UNK (By similarity).
-!- SUBUNIT: Associates with TRAFI, TRAF2, TRAF3, TRAF5 and TRAF6 (By
                             MEDLINE-99061155; PubMed-9846698;
Madry C., Laabi Y., Callebaut I., Roussel J., Hatzoglou A.,
Le Coniat M., Mornon J.P., Berger R., Tsapis A.;
"The characterization of murine BCMA gene defines it as a new member
of the tumor necrosis factor receptor superfamily.";
Int. Immunol. 10:1693-1702(1998).
STRAIN=BALB/c; TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences."
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SUBCELLULAR LOCATION: Type III membrane protein (Probable). ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;

similarity)

Name=1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
               Name=2;
IsoId=088472-2; Sequence=VSP_006507;
TISSUS SPECIFICITY: Detected in spleen, thymus, bone marrow and
heart, and at lower levels in kidney and lung.
                                                                                                                                                                                                                                                                                                                                                                                                                   Signal-anchor for type III membrane protein (Potential).
Cytoplasmic (Potential).
TNFR-Cys.
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
/FTIG=VSP 006507.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tomasetto C., Masson R., Wendling C., Lefebvre O., Chenard M.P.,
                                                                                                                                                                                                                                                                                                                           HSSP; Q02223; 10QD.
MGD; MGI:1343050; Tnfrsf17.
Alternative splicing; Immune response; Receptor; Signal-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 185;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tomasetto C.L.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJO1072; CAA09343.1; -.
MGD; MGI:2663233; Muc6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                        Extracellular (Potential)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  499 AA.
                                                                                        -!- SIMILARITY: Contains 1 TNFR-Cys repeat.
IsoId=088472-1; Sequence=Displayed;
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01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-MAR-2004 (TrEMBLrel. 26, Last anno
Gastric mucin-like protein (Fragment)
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Interpro; IPR001846; VWF_D.
Pfam; PF01826; TIL; 1.
Pfam; PF00094; VWD; 1.
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Local Similarity 70.6%;
nes 24; Conservative
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Matches
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gel-forming mucin gene cluster between human and mouse.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                      36.1%; Score 72.5; DB 2; Length 499; 48.3%; Pred. No. 0.37;
                                                                                                                                                                                                                                                                7; Indels
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                                                                                                             54190 MW; 04F89EF4F23EE61E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escande F., Buisine M.P.;
"The mouse secreted gel-forming mucin gene cluster.";
Biochim. Biophys. Acta 1676:240-250(2004).
EMBL; AJ511867; CAD54415.1; --
EMBL; AJ511868; CAD54415.1; --
INTERPO: IPRO02919; Cyprich TIL.
InterPro: IPRO09041; PMP SGCI.
InterPro: IPRO09041; PMP SGCI.
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                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     1 CSQNEYFDSLLHACIPCOLRCSSNTPPLT 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted gel-forming mucin (Fragment).
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MEDLINE=22563400; PubMed=12676567;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.1%;
48.3%;
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(TrEMBLrel. 24, I
(TrEMBLrel. 26, I
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Best Local Similarity 48.3
                                                                                                                                                                                                                                                                14; Conservative
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SMART; SM00216; VWD; 1.

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SEQUENCE 499 AA; 5419
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                                                                                                                                                                                                                             Local Similarity
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MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

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Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

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Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
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MEDLINE21177554; PubMed=10881172; DOI=10.1038/76889;
MEDLINE22177554; PubMed=10881172; DOI=10.1038/76889;
Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;
"Identification of a receptor for BLyS demonstrates a crucial role in humoral immunity.";
Nat. Immunol. 1:37-41(2000).
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 13B (Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.1%; Score 72.5; DB 2; Length 2850;
48.3%; Pred. No. 2.3;
tive 1; Mismatches 7; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; Prouss, v..., SMART; SM0216; VWD; 3.
PROSITE; PS0125; CTCK 2; 1.
PROSITE; PS0125; CTCK 2; 1.
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EMBL; AY184388; AAO47735.1; -
EMBL; AY184385; AAO47735.1; -
EMBL; AY184387; AAO47735.1; JOINED.
EMBL; AY184386; AAO47735.1; JOINED.
HSSP; O46162; IKNO.
HSSP; O46162; IKNO.
HSSP; IRNO02919; Cygrich TIL.
InterPro; IRNO02919; Cygrich TIL.
InterPro; IRNO02919; Cygrich TIL.
InterPro; IRNO02919; Cygrich TIL.
InterPro; IRNO01941; PMP SGCI.
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Best Local Similarity 48.3
Matches 14; Conservative
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Pfam; PF00094; VWD; 3.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMEL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lb.sib.ch).
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Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kalley M.,
Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,
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"TACI is a TRAFF intersacting receptor for TALL-1, a tumor necrosis
factor family member involved in B cell regulation.";
J. Exp. Med. 192:137-143(2000).
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Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D.,
Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.;
"TACI-1igand interactions are required for T cell activation and
collagen-induced arthritis in mice.";
Nat. Immunol. 2:632-637(2001).
Nat. Immunol. 2:632-637(2001).
Ithat binds both ligands with similar high affinity. Mediates
calcineurin-dependent activation of NP-AT, as well as activation
of NF-kappa-B and AP-I. Involved in the stimulation of B- and T-
cell function and the regulation of humoral immunity (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF257673; AAG00081.1; -.

R EMBL; AK004668; BAB23457.1; -.

R MGD; MG1:189411; Thirsfilb.

R GO; GO:0005031; Fitumor necrosis factor receptor activity; IDA.

R GO; GO:0005031; Fitumor necrosis factor receptor activity; IDA.

R ROSITE; PS00652; TNFR NGFR 1; FALSE NGG.

R PROSITE; PS00652; TNFR NGFR 1; FALSE NGG.

R PROSITE; PS50050; TNFR NGFR 2; FALSE NGG.

M Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.

I DOWAIN 129 149 Signal-anchor for type III membrane process.

I DOWAIN 150 249 CYtoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLG with its C-terminus (By similarity).
SUBCELLULAR LOCATION: Type III membrane protein (Probable).
SIMILARITY: Contains 2 TNFR-Cys repeats.
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CB2F2D61C2931D81 CRC64;
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TWER-Cys 2.

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249 AA;
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CONFLICT
SEQUENCE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                           Rousseau K., Byrne C., Kim Y.S., Gum J.R., Swallow D.M., Toribara N.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomics 83:936-939(2004).
EMBL, AY312160; AAQ82434.1; -.
NON TER 1569 1569 168065 MW; GAEDEE143ECB855B CRC64;
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                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-APR-2004 (TrEMBLrel. 27, Last sequence update) 23-APR-2004 (TrEMBLrel. 27, Last annotation update)
                6 CPKDQYWDSSRKSCVSCALICSQRS-QRICIDFC 38
 1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1179 CSÓDEYFDHEEGVCVPCM-----PPTTPQ 1202
                                                                                                          PRT; 1569 AA.
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INTERPTO; IPR002919; Cystich TIL.
INTERPTO; IPR002919; Cystich TIL.
INTERPTO; IPR001944; WWC OUT.
INTERPTO; IPR001846; VWF_D.
FEam; PP01826; TIL, 2.
FEam; PP010826; TIL, 2.
FEam; PP00094; VWD; 3.
SWART; SW00215; VWC_OUT; 2.
SWART; SW00215; VWC_D; 3.
NON TER 1569 AA; 168065 MW; 6Al
                                                                                                                                                                                     Mucin glycoprotein (Fragment).
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Best Local Similarity 45.2
Matches 14; Conservative
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                                                                                                         PRELIMINARY;
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PubMed=15081123;
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                                                                                                                                                                                                     Name=MUC6;
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AAQ82434;
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                                                                                                                           Q6W4X9;
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                                                                          RESULT 9
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Gaps

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35.6%; Score 71.5; DB 1; Length 249; larity 35.3%; Pred. No. 0.24; Conservative 8; Mismatches 13; Indels 1

Similarity

Query Match Best Local Simi Matches 12;

Best Loca Matches

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POK552; Q62040;

Q04552; Q62040;

Q04552; Q62040;

G1-FBB-1995 (Kel. 31, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

O5-JUL-2004 (Rel. 44, Last annotation update)

Proprotein convertase subtilisin/kexin type 5 precursor (BC 3.4.21.-)

(Proprotein convertase PC5) (Subtilisin/kexin-like protease PC5) (PC6)

(Subtilisin-like proprotein convertase 6) (SPC6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakagawa T., Murakami K., Nakayama K.;
"Identification of an isoform with an extremely large Cys-rich region
of PC6, a Kex2-like processing endoprotease.";
FEBS Lett. 327:165-171(1993).
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                                                                         Gaps
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Constam D.B., Calfon M., Robertson B.J.;
SPC4, SPC6, and the novel protease SPC7 are coexpressed with bone
morphogenetic proteins at distinct sites during embryogenesis.";
J. Cell Biol. 134:181-191(1996).
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MEDLINE=33342056; PubMed=8341687;
Lusson J., Vieau D., Hamelin J., Day R., Chretien M., Seidah N.G.;
"CDNA structure of the mouse and rat subtilisin/kexin-like PC5: a
candidate proprotein convertase expressed in endocrine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97103178; Pubmed-8947550; B., Lazure C., Nakayama K., Ben Bie I., Marcinklewicz M., Malide D., Lazure C., Nakayama K., Bendayan M., Seidah N.G. "The isoforms of proprotein convertase PC5 are sorted to different
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification and functional expression of a new member of the mammalian Kex2-like processing endoprotease family: its striking structural similarity to PACE4.";
                                                                         7;
      2; Length 1569;
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MEDLINE-93224489; PubMed-8468318;
Nakagawa T., Hosaka M., Torii S., Watanabe T., Murakami K.,
                                                                         Indels
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STRAIN=ICR; TISSUE=Intestine;
MEDLINE=93327934; PubMed=8335106;
                                                                                                                                                                              1179 CSQDEYFDHEEGVCVPCM-----PPTTPQ 1202
      B
                                                                                                                                       1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQ 31
34.1%; Score 68.5; D 45.2%; Pred. No. 4.1; ative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM PCSA).
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MEDLINE=97436919; PubMed=9291583;
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                                                                     14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Query Match
Best Local Similarity
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Name=FC54; Synonyme=Long;

Locid=Q04592-1; Sequence=Displayed;

Name=FC54; Synonyme=Long;

CC -1- TISQUE SPECIFICITY: PC5A is expressed in most tissues but is most abundant in the intestine and adrenals. PC5B is expressed in the abundant in the intestine and drenals. PC5B is expressed in the abundant in the intestine and drenals. PC5B is expressed in the intestine, adrenals and lung but not in the brain.

CC -1- DEVELOPMENTAL STAGE: Weakly expressed throughout the embryo, except in the developing nervous system, the ribs and the liver, cc but markedly up-regulated at discrete sites during development. At E5.5, prominent expression observed in differenciated decidua. At E7.5, intense expression in observed in differenciated decidua. At E7.5, intense expression in codermal and somites and yolk sac followed by a confination to dermamyotome compartment. Between E9.5 and E11.5, abundant expression in AER (thickened ectodermal crolls of limb buds). At E12.5, expression in the limbs is confined to the condensing mesenchym surrounding the cartilage. At this stage, strong expression also detected in vertebral and facial cartilage primordia and in the muscle of the tongue. At E15.5, abundant expression in epithelial cells of the intestinal villi. Isoform B occur at E12.5.

-1 DOMAIN: The propeptide domain acts as an intramolecular chaperone assisting the folding of the zymogen within the endoplasmic contains.

--- DOMAIN: The propeptide domain acts as an intramolecular chaperone contains.

--- DOMAIN: The propeptide domain acts as an intramolecular chaperone contains.

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FUNCTION: Likely to represent a widespread endoprotease activity within the constitutive and regulated secretory pathway. Capable of cleavage at the RX(K/R) consensus motif. May be responsible for the maturation of gastrointestinal peptides. May be involved in the cellular proliferation of adrenal cortex via the activation of growth factors.

CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg.-Kaa-Yaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys.

SUBCELLULAR LOCATION: PC5A is secreted through the regulated a gecretory pathway. PC5B is a type I membrane protein localized to a paranuclear post-Golgi network compartment in communication with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sorting information. AC 1 directs TGN localization and interacts with the TGN sorting protein PACS-1.
-!- SIMILARITY: Belongs to peptidase family S8.
-!- SIMILARITY: Contains 1 homo B/P domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- DOMAIN: AC 1 and AC 2 (clusters of acidic amino acids) contain
                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR000209; Pept S8 S53.
Interpro; IPR009020; Prot inh propept.
Interpro; IPR002884; PrproinconvertsP.
Pfam; PF00757; Purin-like; 2.
Pfam; PF00082; Peptidase S8; 1.
Pfam; PF00082; Peptidase S8; 1.
Pfam; PF00083; Puroprotein; 1.
PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI 97515; PoskS.
InterPro; IPR006211; Furin-like.
InterPro; IPR0109010; Grow fac_recept.
InterPro; IPR011031; Multihaem_cyt.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=PC5B; Synonyms=Long;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D17583; BAA04507.1; -. EMBL; D12619; BAA02143.1; -. EMBL; L14932; AAA74636.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A48225; A48225.
PIR; S34583; S34583.
HSSP; P23188; 1P8J.
                                                                                                                                                                                                                                                                                                                                       early endosomes
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'NF-AT activation induced by a CAML-interacting member of the tumor

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N-linked (GlCNAC...) (Potential).
N-linked (GlCNAC...) (Potential).
N-linked (GlCNAC...) (Potential).
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N-linked (GlCNAC...) (Potential).
GEXIDDGGHCCTERACAKCWGFTGEDCISCPATRUD.->
ATERSWAEGGGFCMINKENNICQRKVLQQLCCTTFQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEE-2003 (Rel. 41, Created)
28-FEE-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
1-Wmor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor)
Name=TNFRSF13E; Synonyms=TACI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                  Proprotein convertase subtilisin/kexin
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                                                                                                                                                                                                                                                                   Charge relay system (By similarity)
Charge relay system (By similarity)
Charge relay system (By similarity)
                                                                                                                                                                                                                                                                                                           (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5,
                                                                                                                                                                                                                                           Cleavage (auto-) (By similarity)
Cell attachment site (Potential)
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                                                 Alternative splicing, Cleavage on pair of basic residues;
Direct protein sequencing; Glycoprotein; Hydrolase; Repeat;
Serine protease; Signal; Transmembrane; Zymogen.
                                                                                                                                                                                                   Cys-rich motif (CRM) region.
AC 1.
AC 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 6.7;
4; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EC850E2DF20EA1C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FIId=VSP 005438.
Missing (In isoform PC5A).
                                                                                                                               type 5.
Extracellular (Potential).
Potential.
                                                                                                                                                                 Cytoplasmic (Potential).
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N-linked (GlcNAc. ..)
N-linked (GlcNAc. ..)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoform PC5A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 67.5;
ProDom; PD000717; P_domain; 1.
PROSITE; PS00136; SUBTILASE ASP; 1.
PROSITE; PS00138; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE_HES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1877 AA; 209287 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.6%;
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Best Local Similarity 37.8
Matches 14; Conservative
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                                                                                                                  1877
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T13X HUMAN
ID T13X HUMAN
AC 014836;
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TRANSMEM
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CARBOHYD
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TISSUE=B-cell; MEDLINE=97458245; PubMed=9311921; Von Buelow G.-U., Bram R.J.;

SEQUENCE FROM N.A.

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MEDLINE=20341628; PubMed=1088053; Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R., Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J., Meng S.Y., Boyle W.J., Hau H.; Stolina M., Yu G., Wang J., Delaney J., Meng S.Y., Boyle W.J., Hau H.; Stolina M., Yu G., Wang J., Delaney J., Meng S.Y., Boyle W.J., Hau H.; Stolina M. Gall-regulation."; Tactor family member involved in B cell regulation."; J. Exp. Med. 192:137-143(2000).

J. Exp. Med. 192:137-143(2000).

J. Exp. Med. 192:137-143(2000).

J. Exp. Med. 192:137-143(2000).

J. Exp. Med. 192:137-143(2000).

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J. Exp. Med. 192:137-143(2000).

J. Exp. Med. 192:137-143(2000).

J. Exp. Med. 192:137-143(2
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-1- SIMILARITY: Contains 2 THRE-Cys repeats.
-1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yu G., Boone T., Delaney J., Hawkins N., Kelley W., Ramakrishnan M., McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M., Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.; "APRIL and TalL-I and receptors BCMA and TACI: system for regulating humoral immunity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200; Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K., Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dinke D., LaFleur D., Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J., Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.; Tumor necrosis factor (TMF) receptor superfamily member TACI is a high affinity receptor for TNF family members APRIL and BLyS."; J. Biol. Chem. 275:35478-35485(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                           necrosis factor receptor superfamily.";
Science 278:138-141(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Immunol. 1:252-256(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                               TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION.
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Gaps

5.

Indels

13;

5; Mismatches

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nterPro; IPR001846; VWF_D
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  Conservative
                                                                                              PRELIMINARY;
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PROSITE; PS01186; EGF
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SEQUENCE FROM N.A.
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SMART; SM00274;
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SMART; SM00214;
SMART; SM00216;
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Miller W., K
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use by non-profit institutions as long as its content is in no way additied and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                             . ., TAS.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                           MIM; 604907; -. Golden and membrane; TAS. GO; GO:0005887; C:integral to plasma membrane; TAS. GO; GO:0004872; F:receptor activity; TAS. GO; GO:0007166; P:cell surface receptor linked signal transdu. InterPro; IPR001368; TNFR CS. PROSITE; PS00652; TNFR NGFR 1; 1. PROSITE; PS50050; TNFR NGFR 1; 1.
                                                                                                                                                                                                                                                                                                                       . .) (Potential)
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                                                                                                                                                                     Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%; Score 65.5; DB 2; Length 1025; 36.1%; Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                   Score 66.5; DB 1; Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLP 170 141434 144511.
Giardia lamblia ATCC 50803.
Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
                                                                                                                                                                                        Extracellular (Potential).
Signal-anchor for type III mprotean (Potential).
Cytoplasmic (Potential).
TNFR-Cys 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AACBOLO00001; EAA43000.1; -.
InterPro; IPR000345; CytC_heme_BS.
InterPro; IPR002249; Lamilin EGF.
PROSITE; PS00190; CTCCRPOME_C; UNKNOWN 2.
PROSITE; PS01248; LAMININ TYPE EGF; UNKNOWN 1.
SEQUENCE 1025 AA; 109044 MW; 36281DF3FEZDDB43 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                             411799F3DE17A5EB CRC64;
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Last sequence update)
Last annotation update)
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By similarity.
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No similarity.
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                                                   EMBL, AF023614; AAC51790.1; -. EMBL, BC028072.1; -. HSSP; Q9Y275; 10QD. Genew; HGNC:18153; TNFRSF13B.
                                                                                                                                                                                                                                                                                                                                                31816 MW;
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                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
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104
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DISULFID
CARBOHYD
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"Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5."; Nucleic Acids Res. 29:1352-1365(2001).
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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PROSITE; PS50066; MAM 2; 3.
EGF-like domain; Glycoprotein.
SEQUENCE 5374 AA; 579545 MW; 90D2D8CFESDE24EB CRC64;
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Cheung T.L., Wilson M.D., Koop B.F., Hardy D.M.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 EGF-like domain.
-!- SIMILARITY: Contains 3 MAM domains.
EMBL; AR312033; AAK28824.1; --
EMBL; AY046.65; AAL04416.1; --
HSSP; Q90248; 1HX2.
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Last sequence update)
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1 CSQNEYFDSLLHACIPCQLRCSSNTPP----LTCQ 31
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1 Similarity 35.1%; Pred. No. 50;
13; Conservative 5; Mismatches
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0007339; P:binding of sperm to zi
GO; GO:0007155; P:binding of sperm to zi
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR002919; Cysrich TIL.
InterPro; IPR006209; EGF 2.
InterPro; IPR006209; EGF 7:
InterPro; IPR005210; IEGF.
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01-JUN-2001 (TrEMBLrel. 17,
05-JUL-2004 (TrEMBLrel. 27,
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                   1. SUBGELLULAR LOCATION: Type I membrane protein, exclusively on the apical region of the speam head.
1. SUBCELULAR LOCATION: Type I membrane protein, exclusively on the apical region of the speam head.
1. TASSUE SPECIFICITY: In testis, primarily in haploid spermatids.
1. DOWAIN: The MAM domains probably mediates sperm adhesion to the zona pellucida.
1. DOWAIN: During sperm migration through the reproductive tracts, the mucin-like domain might inhibit inappropriate trapping of spermatozea or promoting adhesion to the oviductal isthmus.
1. DOWAIN: The VWFD domain 2 may mediate covalent oligomerization (By
                                                                                                                                                                                                                                                                                                               MEDLINE-97271566; PubMed=9126492;

Gao Z., Harumi T., Garbers D.L.;
"Chromosome localization of the mouse zonadhesin gene and the human zonadhesin gene (ZAN).";
Genomics 41:119-122(1997).
-I- FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or
                                                                                                                                                                                                              TISSUE-Testis;
MEDLINE-9813114; PubMed-9452463;
Gao Z., Garbers D.L.; the structure of zonadhesin, a sperm-specific membrane protein containing multiple cell adhesion molecule-like
                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                   3298 CPTNSQFTDCLPSCVPSCSNRCEVTSPSVPSSCREGC 3334
        CSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 34
                                                     EESULT 15
ZAN MOUSE
ID ZAN MOUSE
STANDARD; PRT; 5376 AA.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2004 (Rel. 45, Last annotation update)
DT 20-0CT-2004 (Rel. 45, Last annotation update)
DE Zonadhesin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 1 EGF-like domain. SIMILARITY: Contains 3 MAM domains. SIMILARITY: Contains 25 VWFD domains.
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InterPro; IPR002919; Cysrich TIL.
InterPro; IPR00142; EGF 2.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR001938; MAM.
InterPro; IPR001328; TILa.
InterPro; IPR001846; VWF.D.
                                                                                                                                                                                                                                                                 domains.";
J. Biol. Chem. 273:3415-3421(1998)
                                                                                                                                                                                                                                                                                           SEQUENCE OF 4864-5376 FROM N.A.
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EMBL; U83190; AAC53125.1; -.
PIR; T42215; T42215.
HSSP; Q90248; 1HX2.
                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                    SEQUENCE FROM N.A.
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Cytoplasmic (Potential).

MAM 1.

MAM 2.

MAM 3.

NA HEPTAPEPTIDE REPEATS (APPROXIMATE)

(MUCIN-LIKE DOMAIN).
PFam; PF00008; EGF; 1.

Pfam; PF00629; MAM; 35.

R Pfam; PF01826; TIL, 25.

R Pfam; PF00094; WUD; 4.

R PFO0094; WUD; 4.

R PROSITE; PS00186; EGF_1; 1.

R PROSITE; PS00186; EGF_2; 18.

R PROSITE; PS0006; EGF_3; 1.

R PROSITE; PS0006; EGF_3; 1.

R PROSITE; PS0006; EGF_3; 1.

R PROSITE; PS0006; MAM_1; PALSE_NEG.

R PROSITE; PS0006; MAM_2; 3.

R Cell adhesion; EGF-like domain; Glycoprotein; Repeat; Signal; Gransmembrane.
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Zonadhesin.
Extracellular (Potential).
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VWFD 5 (partial).
VWFD 6 (partial).
VWFD 6 (partial).
VWFD 9 (partial).
VWFD 10 (partial).
VWFD 11 (partial).
VWFD 11 (partial).
VWFD 12 (partial).
VWFD 13 (partial).
VWFD 14 (partial).
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By similarity.
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matode C. elegans: a platform for C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                   Wilson R.; Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                 Geisel C.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                Waterston R.; Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
PROSITE; PS00272; SNAKE_TOXIN; UNKNOWN_1.
HYDOTCHE:1021 Protein:
SEQUENCE 966 AA; 102460 MW; BS65A3CDD25216D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.3%; Score 61; DB 2; Le
37.5%; Pred. No. 24;
iive 7; Mismatches 11;
                                                                 "Genome sequence of the nematode C. elegans: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
29-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSQNEYFDSLLHACIPCOLR--CSSNTPPLTC 30
                                                                                                                                                                                                                                                                                                                                                            GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0006061; F: chitin binding; IEA.
GO; GO: 0006030; P: chitin bind_PerA.
InterPro; IPR005257; Chitin_bind_PerA.
InterPro; IPR000794; Ketoacyl_synth.
InterPro; IPR00079571; Snake toxin.
InterPro; IPR0007571; Snake toxin.
InterPro; IPR005771; Snake toxin.
InterPro; IPR00577; CM Morm_repeat_1.
Pfam. PF01607; CMM 14; 2.
SMART; SW00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    867 AA.
                                       MEDLINE=99069613; PubMed=9851916;
                                                                              investigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                       HSSP; P10969; 1WGT.
WormPep; T10E10.4; CE25989.
                                                                                                                                                                                                                                                                                                            EMBL; U39644; AAA80360.2;
PIR; T16840; T16840.
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les 12; Conserv
                                                                                                                                    STRAIN-Bristol N2;
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                          STRAIN=Bristol N2;
                                                                                                                     SEQUENCE FROM N.A.
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                                                      Wilson R.;
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-Stock d4-2;
Zagulski M., Nowak J.K., Le Mouel A., Nowacki M., Migdalski A.,
Gromadka R., Noel B., Blanc I., Dessen P., Wincker P., Keller A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cohen J., Meyer E., Sperling L.;
"High coding density on the largest Paramecium tetraurelia somatic chromosome.";
Curr. Biol. 0:0-0(2004).
                                                                                                                                                                                                                                                                                                                                       01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last amontation update)
Putative surface protein with EGF domains and furin-like repeats.
                                                                                                                                                                                                                                                                                                                                                                                          ORFNames=PTMB.409;
Paramecium tetraurelia.
Bukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                      (Potential)
                                         (Potential)
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                                                                                                                                                              32.1%; Score 64.5; DB 1; Length 5376;
                                                                                                                                                                                       16; Indels
                                                                                                                                   0E44DB77DF2A2620 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nowak J.K., Migdalski A., Gromadka R., Zagulski M.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR548612; CAH03606.1;
SEQUENCE 3005 AA; 343821 WW; DBCCGA247876A5A5 CRC64;
                                                                                                                                                                                                                                 3300 CPINSOFIDCLPSCVPSCSNRCEVISPSVPSSCREGC 3336
                                                                                          (GlcNAc. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                              (GlcNAc. . .
                                         CNAC. . .
                                                                 (GlcNAc. . .
                                                                                                                                                                                                                1 CSQNEYFDSLLHACIP-CQLRCSSNTP--PLTCQRYC 34
                                                      (GlcNAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1190 YFESSTNQCIQCDLSC----FTCQGSSKYC 1215
                                                                                                                      (GlcNAc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 YFDSLLHACIPCQLRCSSNTPPLTCQ---RYC 34
                                                                                                                                                                                                                                                                                                              PRT; 3005 AA
                                                                                                                                                                                       5; Mismatches
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                                                                                                                                  5376 AA; 579908 MW;
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01-OCT-2001 (TrEMBLrel. 18, La
01-MAR-2004 (TrEMBLrel. 26, La
Hypothetical protein T10E10.4.
                                                                                                                                                                          35.1%;
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                                                                                                                                                                                       13; Conservative
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Best Local Similarity 40.6
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                     4243
4254
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Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=Stock d4-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5888;
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                                       4243
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Q6BFG4
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TISSUE-Ependymocyte;
MEDLINE-96338614; PubMed-8743952;
Gobron S., Monnerie H., Meiniel R., Creveaux I., Lehmann W.,
Lamalle D., Dastugue B., Melniel A.;
"SCO-spondin: a new member of the thrombospondin family secreted by
the subcommissural organ is a candidate in the modulation of neuronal
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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Gaps

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Length 966; Indels

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PRT; 5146 AA.
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96 VFHACVPCPLTCDDISGQATC 116
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Subcommissural organ;
MEDLINE=20465125; PubMed=11008217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PP07546; EMI; 1.
Ffam; PP00754; FS F8 LYDe_C; 1.
Pfam; PP00057; Ld_recept_a; 10.
Pfam; PP05375; Pacifastin_I; 1.
Pfam; PP08095; TIL; 10.
Pfam; PP00095; TWC; 1.
Pfam; PP00094; VWC; 1.
Pfam; PP00094; VWC; 1.
Pfam; PP00094; VWC; 1.
SMART; SM00211; PAS8C; 1.
SMART; SM00041; CT; 1.
                                                                                                     10 LLHACIPCOLRCSSNTPPLTC 30
                                                                 Query Match
Best Local Similarity 42.9%;
Matches 9; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Subcommissural organ;
                                                                                                                                                                  Q8SPM4 PRELIMINARY;
Q8SPM4;
01-JUN-2002 (TEMBLE-21,
01-JUN-2002 (TEMBLE-21,
01-MAR-2004 (TEMBLE-1, 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001007; VWF C. InterPro; IPR001846; VWF_D.
                                                                                                                                                                                                                          Name=sco-spondin;
Bos taurus (Bovine).
                                                867 AA;
                                                                                                                                                                                                                  SCO-spondin.
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SEQUENCE
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Q8SPM4
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                       J. Cell Sci. 109:1053-1061(1996).

J. Cell Sci. 109:1053-1061(1996).

J. CHILL SCHECKTON: Involved in the modulation of neuronal aggregation.

J. SUBCELLULAR LOCATION: Extracellular.

J. SINE SPECTFFCITY: Subcommissural organ.

J. SIMILARITY: Belongs to the thrombospondin family.

J. SIMILARITY: Contains at least 2 EGF-like domains.

J. SIMILARITY: Contains at least 1 F5/8 type C domain.

J. SIMILARITY: Contains at least 3 LDL_receptor class A domains.

J. SIMILARITY: Contains at least 4 TSP type-1 domains.

SIMILARITY: Contains at least 4 TSP type-1 domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VAFC.

LDL-receptor class A 1.

LDL-receptor class A 2.

LDL-receptor class A 3.

LSP type-1 3.

TSP type-1 4.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartlodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
MCBI_TaxID=9913;
By similarity.
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
N-linked (GlcNAc. . .) (Potential)
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ416457; CAC94914.1;
HSSP; P98162, IXTB.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0001155; P:cell adhesion; IEA.
InterPro; IPR002919; Cystron IEA.
InterPro; IPR00207; Cys knot C.
InterPro; IPR01489; EMI.
InterPro; IPR004545; GJY hormoneB.
InterPro; IPR0041545; GJY hormoneB.
InterPro; IPR004545; GJY hormoneB.
InterPro; IPR009541; PASB.
InterPro; IPR009541; PASB.
InterPro; IPR009541; PASB.
InterPro; IPR009545; TSPI.
InterPro; IPR008037; Prot_inh_PMP.
InterPro; IPR00884; TSPI.
                                                                                                                                                                                                             Score 60; DB 1; Length 867;
Pred. No. 29;
3; Mismatches 9; Indels
                                                                                                                                                      91817 MW; 9538F2108E787B49 CRC64;
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Last annotation update)
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Lewis S.E.;
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Adams M.D., Cellniker S.E., Li P.W., Hoskins R.A., Gazle R.F.,
Adams M.D., Cellniker S.E., Li P.W., Hoskins R.A., Gazle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gazle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gazle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Gazle R.F.,
Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
Briton G.G., Wordman J.R., Yandell M.D., Zhang O., Chen, L.X.,
Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
Amanatides P.O., Baxter E.G., Helt G., Nelson C.R., Galdwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barwalde J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chante I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chanter S.,
Burtis K.C., Busam D.A., Butler H., Dugan-Rocha S., Dunkov B.C., Dunn P.
Burtis K.C., Busam D.A., Butler H., Dugan-Rocha S., Dunkov B.C., Dunn P.
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P.
Burtis N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Anderin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
Alalli M., Kalluh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalluh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Basko P., Lei Y., Leivisky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., MoIntosh T.C., Moiris J., Moshrefi A.,
Balazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
Rahen B.C., Siden-Kiamos I., Shupson M., Strong R., She H.,
Shire B., Spieraling A.C., Stapleton M., Strong R., Shir H.,
Spier B., Soler E., Spierdling A.C., Turner R., Venter E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                          Gaps
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                          PROSITE; PS01225; TCCK 2; 1.
PROSITE; PS01285; FA58C 1; UNKNOWN 1.
PROSITE; PS01286; FA58C 2; 1.
PROSITE; PS01286; FA58C 3; 1.
PROSITE; PS01209; LDLRA 1; 7.
PROSITE; PS00261; GLYCO HORMONE BETA 1; 2.
PROSITE; PS0002; TSP1, 22; PROSITE; PS0002; TSP1, 22; PROSITE; PS01209; UDLRA 2; 9.
PROSITE; PS01208; VWFC 2; UNKNOWN 1.
PROSITE; PS01208; VWFC 2; 2.
PROSITE; PS01208; VWFC 2; 2.
SEQUENCE 5146 AA; 543588 MW; 724C5FB8727E13DA CRC64;
                                                                                                                                                                                                                              29.9%; Score 60; DB 2; Length 5146; 42.9%; Pred. No. 1.9e+02; ive 3; Mismatches 9; Indel8
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                   353 AA
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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1814 VFHACVPCPLTCDDISGQATC 1834
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9; Conservative
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Best Local Similarity
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01-MAY-2000
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
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MEDLINE=22426069; PubMed=12537572;
Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drygadle R.N.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
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PlyBase; PBGn0036940; CG7348.
GO; GO: 0005576; C: extracellular; IEA.
GO; GO: 0006030; P: chitin binding; IEA.
GO; GO: 0006030; P: chitin bind_PerA.
InterPro; IPR002557; Chitin_bind_PerA.
SMART; SM00494; CHED2; 3
PROSITE; PS50940; CHIT BIND II; 4.
SROUENCE 353 AA; 39713 MW; 1C66916504FD130B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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Local Similarity 31.8%; Pred. No. 13;
les 14; Conservative 4; Mismatches
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neopiera; Endopieraygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY071103; AAL48725.1; -..
Flybase; EBgn0038940; GG7348.
GO; GO:000576; C:extracellular; IEA.
GO; GO:0008061; F:chitin binding; IEA.
GO; GO:000807; P:chitin binding; IEA.
InterPro; IPR002557; Chitin_bind_PerA.
Fam; PF01607; CBM 14; 4:
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                             Last sequence update)
Last annotation update)
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01-007-2002 (TrEMBLrel. 22, Last sequence update)
01-0AR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ34691.
Homo sapiens (Human).
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31.8%; Pred. No. 13;
ive 4; Mismatches
       Created)
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    01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 31.8'
Matches 14; Conservative
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01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                               ORFNames=CG7348;
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                                                                      RE16222p.
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RA OFA T., SULUKIY Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA OFA T., Suluki Y., Nahikawa T., Otsuki T., Shibahara T., Tanaka T., Ishii S.,

RA Makamattsu A., Hayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Murakami K., Yasuda T., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Abe K., Takibashi T., Yamashita H., Murakawa R., Pujimori K.,

RA Abe K., Kamihara K., Ratsuabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Annomiya K., Takibashi Pujii A., Hara H., Tanase T., Nomura Y.,

RA Annomiya K., Takibashi Pujii A., Hara H., Tanase T., Nomura Y.,

RA Annomiya K., Watsunabe M., Takeuchi K., Anita M., Imose N.,

Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

RA Nomiya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suuki O.,

RA Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Yamazaki M., Watanabe T., Suqiyama A., Takemoto M., Kawakami B.,

RA Hishigaki H., Watanabe T., Sujiyama A., Takemoto M., Chmaya T.,

RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Pujiwara T.,

RA Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Sana K.,

RA Wawabata A., Hikiji T., Kobatake N., Inagaki H., Masahita R.,

RA Abatumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takabashi Y., Nakagawa K.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takabashi Y., Nakagawa K.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takabashi Y., Nakami K., Nakajima Y., Ohara O., Isogai T., Sugano S.,

RA Nakai K., Nakajima Y., Ohara O., Isogai T., Sugano S.,
Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura Y., Ohara O., Isogai T., Sugano S., Nakani K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ34743.
Homo sapiens (Human).
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EMBL, AKO92010; BAG03789.1; -.
InterPro; IPR000859; CUB.
InterPro; IPR009030; Grow_fac_recept.
Pfam; PR00431; CUB; 1.
PROSITE; PS01180; CUB; 1.
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nes 11; Conservative
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SEQUENCE FROM N.A.
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Haich F.,
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Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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Villalon D.K., Murny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Complete sequencing and characterization of 21,243 full-length human
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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                                                                                                                                                                                       Genew; HGNC:13655; CEGF3.
Genew): HGNC:13655; CEGF3.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005509; F:calcium ion binding; IEA.
GO; GO:0004889; F:transmembrane receptor activity; IEA.
GO; GO:0007596; P:blood coagulation; IEA.
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SMART; SM001042; CUB; 1.
SMART; SM00179; EGF CA; 3.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01186; EGF 2; 5.
PROSITE; PS01186; EGF 2; 3.
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InterPro; IPR001881; EGF Ca.
InterPro; IPR001809; EGF Tike.
InterPro; IPR009030; Grow fac rece
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                                                                            Nat. Genet. 36:40-45(2004).
EMBL; AK092062; BAC03798.1; -.
HSSP; P35555; 1LMJ.
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Pfam; PF00008; BGF; 4.
Pfam; PF07645; BGF_CA; 2.
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SEQUENCE 880 A
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Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Attaubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Attaubberg R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Attachul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhar N.K.,

Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Heish F.,

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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W. Touchman, J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Tones S.J., Marra M.A., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,

T. and mouse CDNA sequences.
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032835; AAH32835.1; -.
                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000150; Hypothet_cof.
PROSITE; PS01228; COF_1; UNKNOWN_1.
Hypothetical protein.
PROPENCE 985 A4, 110858 MW; 711109F095C12E89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCERFIC, TOTAL COP 1; UNKNOWN 1. PROSITE; PS01228; COP 1; UNKNOWN 1. 985 AA; 110872 MW; 971B5626C726B3B4 CRC64;
                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.6%; Score 59.5; DB 21.6%; Pred. No. 39; tive 9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.6%; Score 59.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR009030; Grow fac_recept.
InterPro; IPR000150; Hypochet_cof.
PROSITE; PS01228; COF 1; UNKNOWN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22388257; PubMed=12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.6
Best Local Similarity 21.6
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
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Pred. No.

28.98;

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Best Local Similarity 28.9
Matches 11; Conservative
                                                                                                                                        Q81X30
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Q7Z6F5
                                                                                                               RESULT 27
                                                                                                                             QBIX30
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Klausherg R.D., Collins F.S., Wagner L. Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A papteron M., Soares M.B., Bonaldo M.F., Gasavant T.L., Scheetz T.B.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Prange C.,
A Brownstein M.J., Usdin T.B., Tooshiyuki S., Carnhori P., Prange C.,
A Brownstein M.J., Widin T.B., Tooshiyuki S., Carnhori P., Prange C.,
A Brownstein M.J., Wolen P.D., McKernan K.J., Malek J.A., Gunzarene P.H.,
Bosak S.A., McKwam P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,
A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
T "Generation and initial analysis of more than 15,000 full-length human
                   ij
                   Gaps
                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                  12; Indels 19;
                                                           1 CSQNEYFDSLLHACIPC------QLRCSSNTPPLTCQR 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         992 AA; 109165 MW; 24093050738932E1 CRC64;
                                                                                                                                                                   01-MAR-2004 (TrEMBLrel. 26, Last sequence update) Signal peptide, CUB domain, EGF-like 3. Name-SCUBE3; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                       992 AA
                9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC052263; AAH52263.2; -.
GO; GO:0005509; F:calcium ion binding; IEA
    Pred. No. 39;
                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000152; Asx_hydroxyl_S.
                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                TISSUE=Pancreas; MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00042; CUB; 1.
SMART; SM00181; EGF; 10.
SMART; SM00181; EGF; 10.
PROSITE; PS001010; ASK HYDROXYL; 6.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; EGF 2; 7.
PROSITE; PS010187; EGF 2; 7.
PROSITE; PS010187; EGF 2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000859; CUB.
InterPro; IPR000142; EGF 2.
InterPro; IPR0001881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR006210; IEGF.
    21.6%;
                                                                                                                                                            01-JUN-2003 (TrEMBLrel. 24, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00431; CUB; 1.
PF00008; BGF; 4.
PF07645; EGF_CA; 4.
               11; Conservative
                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse cDNA sequences.
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE=Pancreas;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                     Q86UZ9
                                                                                                                                     Q86UZ9
                                                                                                           RESULT 26
Q86UZ9
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                Matches
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Length 992;

DB 2;

29.6%; Score 59.5;

Query Match

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EMBL; AR452494; AAN76808.1; --
HSSP; P35555; 1EMN.
                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.6%; Score 59.5; DB 2; Length 993; 28.9%; Pred. No. 39; ive 5; Mismatches 9; Indels 13
                   9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        993 AA; 109282 MW; 19BBE0E5627EEAF4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang
                                                                                   (TrEMBLrel. 23, Created)
(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | | | | :::: | | | | : CSPGHYYNTSIHRCIRCAMGSYQPDFRQNFCSRCPGNT 786
                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OT-2004 (TrEMBLrel. 26, Last annotation update)
Transmembrane activator and CAML interactor.
Name=TNFRSF13B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CSQNEYFDSLLHACIPCQL------RCSSNT 25
                                                             -----RCSSNT
                                                                                                                                                                                                           993 AA.
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ed. No. 39;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005509; F:calcium ion binding; IEA.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR000859; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMO0042; CUB; 1.

SMART; SMO0042; CUB; 1.

SMART; SMO119; EGF CA; 6.

PROSITE; PS01010; ASX HYDROXYL; 6.

PROSITE; PS01180; CUB; 1.

PROSITE; PS0126; EGF 2; 7.

PROSITE; PS0026; EGF 2; 7.

PROSITE; PS0026; EGF 2; 6.

EGF-1ike domain.

SEQUENCE 993 AA; 109282 MW; 19BBE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000742; EGF 2.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR009030; Grow_fac_recept.
                                                                                                                                                                                                           PRT;
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                 5;
                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 23, Last 01-MAR-2004 (TrEMBLrel. 26, Last CUB and EGF containing protein.
                                                           1 CSQNEYFDSLLHACIPCQL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.6%;
Best Local Similarity 28.9%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00431; CUB; 1.
Pfam; PF00008; EGF; 4.
Pfam; PF07645; EGF_CA; 4.
                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                   01-MAR-2003
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Local Similarity 31.9
      musculus (Mouse)
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                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Appothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                      Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length
enriched library, clone:B230316E19 product:hypothetical protein, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                29.4%; Score 59; DB 2; Length 247; 34.4%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 2; Length 937;
Pred. No. 43;
                                                                          34.4%; Pred. No. 11;
tive 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
   to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
Latreille P., Wohldmann P., Zidanic M.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR009057; Homeodomain_like.
Hypothetical protein.
SEQUENCE 937 AA; 106668 MW; IC140595DFD3ACE4 CRC64;
                                            850E1F4C2578E8E6 CRC64;
                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical protein C23G10.8.
                                                                                                                       29 QGKFYDHLLRDCISCASICGQH--PKQCAYFC 58
                                                                                                        3 QNEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
Submitted (MAY-2003) to the EMBL/GenBank/DDF
EMBL, AY302137, AAP57629.1, -
GO; GO:0016021; C:integral to membrane; IEA.
                                                                                                                                                                                 937 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Mismatches
                                                                                                                                                                                                    Created)
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                                                                                                                                                                                 PRT;
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ESVFHPLYPAEIRCSADGPPL 459
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                                                                                                                                                                                                                                                                                                                                 MEDLINE=99069613; PubMed=9851916;
                                            247 AA; 26664 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U39851; AAF99879.1; -. PIR; T15577; T15577.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 29.4%;
Local Similarity 42.9%;
hes 9; Conservative 6
                                                                                                                                                                                                   (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; C23G10.8; CE25784
                                                                          Local Similarity 34.4 tes 11; Conservative
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                             ORFNames=C23G10.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                                      STRAIN=Bristol N2;
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IntAct; Q9GYR5; -
                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   insert sequence
                                  Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Waterston R.;
                                                                                                                                                                                                    01-MAR-2001
                                                                                                                                                                                                                                                                                                                                            Wilson R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted
                                            SEQUENCE
                                                                 Query Match
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                                                                                                                                                                              Q9GYR5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8BR19
                                                                            Best Loc
Matches
                                                                                                                                                           RESULT 29
Q9GYR5
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QBR19
1D QBR11
AC QBR11
DT 01-MA
DT 01-MA
DT 01-MA
DF 01-MA
DE MUS M
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GTRAIN-CSTBL/61; TISSUE-COIPORA quadrigemina;
A dacchi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A dacchi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
A Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.
A Hayashida K., Hayatsu N., Hirancto K., Hiracka T., Hirozane T.,
A Hori F., Imotani K., Ishii Y., Itch M., Kagawa I., Kasukawa T.,
A Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
A Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakazi K., Sakazume N., Sanno H.,
A Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka I.,
Towar J., Yoya I., Yasunishi A., Muramatsu M., Hayashizaki Y.;
EMBL, AK045875; BAC32518.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs."; Nature 420:563-573 (2002).
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K.,
Fujiwake S., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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STRAIN=CS7BL/6J; TISSUE=Corpora quadrigemina;
The FANTOM Consortium,
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STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;
MEDLINE=99279253; PubMed=10349636;
Carnino: P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ESTBAL/61; TISSUE-Corpora quadrigemina;
MEDLINE-21085660; PubMed=11217851;
RIKEN FANTOM CORSORTIUM;
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SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE STRAIN-C57BL/6J; TISSUE-Small intestine;

MEDINE-25354683; PubMed=1246681; DOI=10.1038/nature01266;

MARAIGA I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Nikaido I., Osato N., Haile D.P., Bult C., Hume D.A., Quackenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Canchenbush J., Baldarelli R., Hill D.P., Bult C., Hume D.A., Chochain C., Corbani L.E., Cousins S., Dalla E., Dragami T.A., Fletcher C.P., Forrest A., Frazer K.S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanaj A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Maghott D.R., Maltedis L., Marchionni L., McKenzie L., Mikh H., Nagashima T., Numata K., Okido T., Pertea G., Percle G., Percle G., Percle G., Percle G., Percle G., Percle G., Percle G., Percle G., Rayasi T., Roed J.C., Reed D.J., Raig J.C., Rodwall R., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Sandelin A., Schneider C., Semple C.A., Vanagiswa M., Yang I., Yang I., Yang I., Yang I., Wanna Z., Zavolan M., Zhumer A., Carninci P., Hayatsu N., Altaxa T., Wanki W., Makawa T., Konno H., Nakawa M., Sakazume N., Sato K., Altaxa A., Hashizume W., Imceani K., Ishii Y., Itoh M., Kagawa I., Rawa A., Hashizume W., Imceani K., Ishiat K., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakazume N., Sakasi M., Wataraki K., Sawasi D., Shibata K., Sakasi D., Shibata K., Sawasi D., Shibata K., Sakasi D., Shibata K., Sakasi D., Shibata K., Sakasi D., Shibata K., Sakasi D., Shibata K., Sakasi D., Shibata K., Sakasi D., Shibata K., Sakasi D., Shibata K., Sakasi D., Shibata K., Shingawa J., Shingawa J., Shingawa J., Shingawa J., Shingawa J., Shingawa J., Shingawa J., Shingawa J., Shingaw
                                                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (BLyS receptor 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21475520; PubMed-11591325;
Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
Canorro M.P., Grewal I.S., Dixit V.M.;
"Identification of a novel receptor for B lymphocyte stimulator that is mutated in a mouse strain with severe B cell deficiency.";
Curr. Biol. 11:1547-1552(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ambrose C.; anewly identified TNF receptor that specifically interacts with BAFF.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Musinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
STRAIN=BALB/C; TISSUB=B-cell lymphoma;
MEDLINE=21442055; PubMed=11509692; DOI=10.1126/science.1061965;
Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
Strauch K., Zafari M., Benjamin C.D., Tschopp J., Browning J.L.,
4 YFNSLLFLSLFCIFKRILTLRCTSHPPPSPPPPPPPPHSHSLACGYFC
                                                                                                                                                                                                                                            175 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (B-cell maturation defect).
Name=Infrsf13c; Synonyms=Baffr, Bcmd, Br3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 293:2108-2111(2001).
                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                           TISOIDE OPDEADO-2; Sequence=VSP 006506; TISOIDE SPECIFICITY: Highly expressed in spleen and testis; detected at lower levels in lung and thymus.

DISEASE: Defects in Thfrell3c are a cause of severe B-cell deficient strain A/WySnJ has a 4.7 kb insertion in the BAFFR gene leading to an altered C-terminus. The mutent RNA is not detectable. B-cells its much reduced. Span of peripheral B-cells its much reduced.

SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                     Harless S.M., Lentz V.M., Sah A.P., Hau B.L., Clise-Dwyer K., Halbert D.M., Hayes C.E., Cancro M.P.; Competition for BLys-mediated signaling through Bcmd/BR3 regulates peripheral B lymphocyte numbers."; Curr. Biol. 11:1986-1989 (2001).

-: FINCTION: B-cell receptor specific for TNFSF13B/TALLI/BAFF/BLyS. Promotes the survival of mature B-cells and the B-cell response.:- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform 2).
/FIId=VSP_006506
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MGD; MGI:1919299; Tnfrsf13c.
Alternative splicing; Glycoprotein; Immune response; Receptor;
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Cytoplasmic (Potential).
TNFR-Cys (incomplete).
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Last annotation update)
                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
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By similarity.
N-linked (GlcNAc.
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                          MEDLINE=21614654; PubMed=11747827;
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DOMAIN
1 71
TRANSMEM 72 92
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01-JUN-2003 (TrEMBLrel. 2.
01-JUN-2003 (TrEMBLrel. 2.
TRAF3 binding protein.
Name-Infrsf13c;
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae; Amphipyrinae; Spodoptera.
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R GO; GO: 0016620; C:membrane; IEA.

R GO; GO: 0016524; F:ATP binding; IEA.

CO; GO: 0016224; F:ATP binding; IEA.

CO; GO: 0016283; F:peptidase activity; IEA.

R GO; GO: 0004214; F:subtidase activity; IEA.

R GO; GO: 0004714; F:transmembrane receptor protein tyrosine kin. .;

R GO; GO: 0006568; P:protein amino acid phosphorylation; IEA.

R GO; GO: 0005508; P:protein amino acid phosphorylation; IEA.

R GO; GO: 0007169; P:protein amino acid phosphorylation; IEA.

R GO; GO: 0007169; P:transmembrane receptor protein tyrosine kin. .;

R InterPro; IPR006211; Furin repeat.

R InterPro; IPR006212; Furin repeat.

R InterPro; IPR000209; Pept_S8 S5.

R InterPro; IPR000209; Pept_S8 S5.

R InterPro; IPR000209; Pept_S8 S5.

R InterPro; IPR000209; Prot_inf propept.

R InterPro; IPR000209; Prot_inf propept.

R Pfam; PF000481; ProprotnonvertsP.

R Pfam; PF00082; Peptidase S8; 1.

R Pfam; PF00082; Peptidase S8; 1.

R RNTS; RN00723; SUBTILISIN.

R SMART; SN00723; SUBTILISIN.

R SMART; SN00721; FU; 10.
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                                                                                                                                                     28.9%; Score 58; DB 2; Length 175; 47.4%; Pred. No. 10;
[1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMITTED (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF350257; AAL83914.1; -.
HSSP; O96RJ3; ADBJ919299; Thfref13c.
MGD; MGI:19192999; Thfref13c.
SEQUENCE 175 AA; 18846 MW; B64EFF4B52EE93B1 CRC64;
                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUB-SE9;
Cleplik M., Klenk H.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: Belongs to peptidase family S8.
-- EMBL, 743281; CAA93116.1; --
PIR; T43221; T43251.
HSSP; P23188; 1P9J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00190; CYTCCHROME C; UNKNOWN 3.
PROSITE; PS00136; SUBTILASE ASP; UNKNOWN 1.
PROSITE; PS00137; SUBTILASE HIS; 1.
PROSITE; PS00138; SUBTILASE ERR; 1.
Hydrolase; Procease; Serine procease.
SEQUENCE 1299 AA; 142019 MW; 4C3799C7BBC572AB CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                        4; Mismatches
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37.1%;
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Best Local Similarity 47.47
Best Local Similarity 67.47
Conservative
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Name=FURIN;
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9; Indels

5; Mismatches

13; Conservative

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                    Babin D.R., Peanasky R.J., Goos S.M.; "The isoinhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the primary structure.";
                                                                                                           TCE1_ASCSU STANDARD; PRT; 63 AA.
P07651; 077419;
01-AUG-1988 (Rel. 08, Last sequence update)
01-AUG-2084 (Rel. 08, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Chymotrypain-delatese isoinhibitor 1 (C/B-1 inhibitor) (ABC/B-1).
Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Bukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=98297373; PubMed=9635450;
Lu C.C., Mguyen T., Morris S., Hill D., Sakanari J.A.;
Anisakis simplex: mutational bursts in the reactive site centers of serine procease inhibitors from an ascarid nematode.";
Exp. Parasitol. 89:257-261(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *APY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE. MEDLINE=95006335; PubMed=7922044; Huang K., Strynadda N.C., Bernard V.D., Peanasky R.J., James M.N.; Huang K., Strynadda N.C., Bernard V.D., Peanasky R.J., James M.N.; Chymotrypsin/elastase inhibitor with porcine elastase."; Structure 2:679-689(1994).
-i- FUNCTION: Defends the organism against the host's proteinases.
-i- SUBCELLULAR LOCATION: Secreted.
-i- SUBCELLULAR LOCATION Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein sequencing; Serine protease inhibitor
                 1 CSQNEYFDSLLHACIPCQLRCS----SNTPPLTC 30
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PD -> DP (in Ref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reactive bond
                                                                                                                                                                                                                                                                                                                                                                                    Arch. Biochem. Biophys. 232:143-161(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U94499; AAC61300.1; -.
PDB; 1EAI; X-ray; C/D=1-61.
InterPro; IPR002219; Cysrich_TIL.
Pfam; PF01826; TIL; 1.
3D-structure; Direct protein seque
DOMAIN 5 60 TIL.
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CONFLICT
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Amanatides P.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Coorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Am K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Péannhoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Dodson K., Doup L.B., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P.,
Dodson K., Doup L.B., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P.,
Porler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Oregon-R, Tuebingen, and Iso-1;
MEDLINE=92381036; PubMed=1512259;
Roebroek A.J.M., Creemers J.W.M., Pauli I.G.L., Kurzik-Dumke U.,
Rentrop M., Gateff E.A.F., Leunissen J.A.M., van de Ven W.J.M.;
RCIOning and functional expression of Dfurin2, a subtilisin-like
proprotein processing enzyme of Drosophila melanogaster with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression during embryogenesis, and pro-protein processing activity of its translational product Dfurin2."; DNA Cell Biol, 14:223-234(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE=55186060; PubMed=7880443;
Roebroek A.J.M., Ayoubi T.A.Y., Creemers J.W.M., Pauli I.G.L.,
van de Ven W.J.M.;
"The Dfurz gene of Drosophila melanogaster: genetic organization,
                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                          1930432; 024301; 028282; 01-ARR-1993 (Rel. 25, Created) 28-FRB-2003 (Rel. 25, Created) 28-FRB-2003 (Rel. 44, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Purin-like protease 2 precursor (EC 3.4.21.75) (Furin 2). Name-Fur2; ORFNames-CG18734; Drosophila melanogaster (Fruit fly). Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Drosophilidae; Drosophila.
                                                                                                                                                   Score 57.5; DB 1; Length 63; Pred. No. 4.1;
                                                                                                                                                                                        Indels
                                                                                                              5DC10DE75B375F16 CRC64;
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                                                                                                                                                                                                                              1 CSQNEYFDSLLHACIPCQLRC--SSNTP-PLTCQR 32
                                                                                                                                                                                                                                                   CGPNEVWTE----CTGCEMKCGPDENTPCPLMCRR 35
                                                                                                                                                                                                                                                                                                                                                                PRT; 1679 AA.
                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deats of a cysteine motif.";
Biol. Chem. 267:17208-17215(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORM D).
                                                                                                            6862 MW;
                                                                                                                                                   28.6%;
                                                                                                                                                                         37.18;
                                                                                                                                                                                        13; Conservative
                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                   Local Similarity
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SEQUENCE OF 305-1679 FROM N.A. (ISOFORM A).

STRAIN=BERKeley; TISSUE=Embryo;

MEDLINE=22426066; PubMed=12537569;

A stapleton M., Carlson J.W., Brockstein P., Yu C., Champe M.,

George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,

A brosophila full-length cDNA resource.";

Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).

-!-FUNCTION: Putin is likely to represent the ubjquitous endoprotease activity within constitutive secretory pathways and capable of activity within constitutive secretory pathways and capable of cleavage at the RX(K/R)R consensus motif (By similarity).

-!-CATALYTIC ACTIVITY: Release of mature proteins from their proproteins by cleavage of Arg-Xaa-Yaa-Arg-|-Zaa bonds, where Xaa can be any amino acid and Yaa is Arg or Lys. Releases albuinh,

COMPLEMENT COMPONENT COMPONENT CAN AND COMPLEMENT COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND COMPLEMENT CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN AND CAN
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Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Adali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Rimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milahina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson B.R., Nelson K., Nixon K., Naskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas K., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J. S., Zhan M., Zhang G., Zhao Q.A.,
A Zheng X.H., Zhong W., Zhong W., Zhou S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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IsoId=P30432-2; Sequence=VSP 009365;
Note=No experimental confirmation available;
ISSUE SPECIFITY: Transient expression in a subset of central
nervous system neurons during embryonic stages 12-13. Expression
in developing tracheal tree from stage 13 to end of embryonic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lewis S.E.; ^{\prime} "Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=D; Synonyms=E;
IsoId=P30432-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 287:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 systematic review.";
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Dunn P., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi B., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theologis A., Ecker J.R., Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Chao Q., Brooks S., Buehler B., Johnson-Hopson C., Khan S., Kim C.,
Shinn P., Altafi H. Bei B., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.
                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                   1198 CSESEFYSQVEGQCRPCHASCGSCNGPADTSCTSC 1232
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     CSONEYFDSLLHACIPCOLRCSS-NTPPLTCORYC
                                                                                                 321 AA
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR011011; FYVE PHD ZnF.
InterPro; IPR010015; Howeodomain like.
InterPro; IPR01005; MyD DNA binding.
InterPro; IPR001965; Znf_PHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00717; SANT; 1.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS50090; MYB_3; 1.
PROSITE; PS01359; ZF_PHD_1; UNKNOWN_1.
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01-MAR-2004 (TrEMBLrel. 26, C
01-MAR-2004 (TrEMBLrel. 26, L
01-MAR-2004 (TrEMBLrel. 26, L
GLP_447_61408_57776.
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12; Conservative
                                                                                                 PRELIMINARY;
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SEQUENCE 321 A
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Charge relay system (By similarity)
Charge relay system (By similarity)
Charge relay system (By similarity)
10 X tandem repeats, Cys-rich.
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Pred. No. 1.2e+02;
5; Mismatches 17; Indels 1
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MW; 3F9E749F0B021CF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L -> LVSK (in isoform A)
/FTId=VSP 009365.
Missing (In Ref. 1).
V -> F (in Ref. 1).
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N-linked (GlcNAc. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
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N-linked
                                         PIR; A43434; A43434.
HSSP; P23188; 1P8J.
MRROPS; S08.049; -.
Flybase; Fsp00004578; Furz.
GO; GO:0004276; F:furin activity; IDA.
InterPro; IPR006211; Furin-like.
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AE003502; AAF48598.2; -.
AE003502; AAN09400.1; -.
AY070553; AAL48024.1; ALT_INIT.
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ilarity 34.3%;
Conservative
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Matches 12; Conserv
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SEQUENCE FROM N.A
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005006; F:epidermal growth factor receptor activity; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0016740; F:transferase activity; IEA.
GO; GO:0016468; P:protein amino acid phosphorylation; IEA.
GO; GO:0007169; P:transmembrane receptor protein tyrosine kin. . .; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schistosoma mansoni (Blood fluke).
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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MEDLINE-92365727; PubMed=1501637;
MEDLINE-92365727; PubMed=1501637;
Shoemaker C.B., Ramachandran H., Landa A., dos Reis M.G., Stein L.;
"Alternative splicing of the Schistosoma mansoni gene encoding a
homologue of epidermal growth factor receptor.";
Mol. Biochem. Parasitol. 53:17-32(1992).
BMB1, M8558, A45588.
HSSP, P11362, 1FGK.
                                                                                                                                                     STRAIN=WB C6;
Morrison H.G., McArthur A.G., Adam R.D., Aley S.B., Gillin F.D., Olsen G.J., Sogin M.L.;
"Draft sequence of the Giardia lamblia genome.";
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 28.4%; Score 57; DB 2; Length 1210; Local Similarity 35.7%; Pred. No. 1e+02; les 15; Conservative 4; Mismatches 9; Indels 1
                          Eukaryota, Diplomonadida, Hexamitidae, Giardiinae, Giardia.
NCBI_TaxID=184922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1210 AA; 132500 MW; 0AC83EEA78A5D726 CRC64;
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01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
pridermal growth factor receptor precursor.
Name=SER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO1415; ANKYRIN.
PROSITE; PS50088; ANK REPEAT; 1.
PROSITE; PS50297; ANK_REP_REGION; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR006212; Furin repeat.
InterPro; IPR009030; Grow Fac recept.
InterPro; IPR01009; Kinase 11ke.
InterPro; IPR000719; Prot Kinase.
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InterPro; IPR008266; Tyr pkinase AS.
InterPro; IPR007087; Znf C2H2.
                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
EMBL; AACROB10000029; EAA41074.1; -.
InterPro; IPR002110; ANK.
Pfam; PF00023; Ank; 23.
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InterPro; IPR000494; EGFR_L.
InterPro; IPR006211; Furin-like.
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Giardia lamblia ATCC 50803
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SEQUENCE
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STRAIN=ATCC 50154;
MEDLINE-21625102; PubMed=11752452;
King N., Carroll S.B.;
A receptor tyrosine kinase from choanoflagellates: molecular insights into early animal evolution.";
Proc. Natl. Acad. Sci. U.S.A. 98:15032-15037(2001).
                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ATCC 50154;
MEDINES22752568; PubMed=12869759;
King N., Hittinger C.T., Carroll S.B.;
"Evolution of key cell signaling and adhesion protein families
                                                                                                                                                                                                                                                                                                             28.4%; Score 57; DB 2; Length 1717; 40.9%; Pred. No. 1.5e+02; tive 2; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 301:361-363(2003),

EMBL, AF440159; AAL33602.2;

O, GO:0005524; F:ATP binding; IEA.

GO; GO:0005509; F:Calcium ion binding; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

InterPro; IPR000742; EGF_2.
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Bukaryota, Choanoflagellida, Codonosigidae, Monosiga.
NCBL_TaxID=81824,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1476 AA.
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InterPro; IPR00181; BGF_Ca.
InterPro; IPR001801; Ig MRC.
InterPro; IPR011009; Kinase like.
InterPro; IPR001019; Prot Kinase.
InterPro; IPR000415; Sushi SCR_CCP.
InterPro; IPR00145; Yyr_Dkinase.
InterPro; IPR001826; Tyr_Dkinase_AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                   CPRNTYIDPQTRHCLPCNESCS 667
                                                                                                                                                                                                                                                                                                                                                                                                       1 CSQNEYFDSLLHACIPCOLRCS 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, 01-OCT-2003 (TrEMBLrel. 25, 01-MAR-2004 (TrEMBLrel. 26, Receptor tyrosine kinase. Name=MBRTK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00084; Sush; 1.
PRINTS; PR0109; TYRKINASE.
ProDom; PD000001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00008; EGF; 2.
Pfam; PF07645; EGF CA; 1.
Pfam; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 40.95
Matches 9; Conservative
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SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                         Query Match
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MEDLINE-22388257; PubMed=12477932;

RETAUBRET R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RIAUSHER R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B.B., Barchow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Pahey J., Helton B., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1476;
                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; EGF-like domain; Kinase; Receptor; Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1476 AA; 157129 MW; BEF0A03DDC3AD897 CRC64;
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Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                        E; PSOU022; BGF_2; 1.

E; PSO1186; BGF_2; 1.

E; PSO1187; BGF_2; 3.

E; PSO1197; BGF_A; 3.

E; PSO0107; PRÖTEIN KINASE ĀTP; UNKNOWN 1.

E; PSO0109; PROTEIN KINASE ĀOP; 1.

E; PSO0109; PROTEIN KINASE ĀOP; 1.

E; PSO0109; PROTEIN KINASE ĀOP; 1.

E; PSO0109; PROTEIN KINASE ĀOP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.1%; Score 56.5; DB 2; Best Local Similarity 35.3%; Pred. No. 1.5e+02; Matches 12; Conservative 4; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 CTISRNFSDLPPSCVPCPLNTARAQDNHAEATCQ 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSONEYFDSLLHACIPCQL---RCSSNTPPLTCQ 31
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STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; BC064748; AAH64748.1; -...
GO; GO:0007276; P:gametogenesis; IDA.
Interpro; IPR007087; Znf_C2H2.
Pfan; PP00096; zf-C2H2; 3.
ProDom; PD000003; Znf_C2H2; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                      PROSITE, PS00010, ASX_HYDROXYL, 1.
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SEQUENCE 1476 AA; 157
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                                                                                                                           PS00022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004
                                                                                                                                                                                       PROSITE;
PROSITE;
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PROSITE;
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Fire the state of Zfp393, a germ cell-specific gene encoding a novel
                                                                                                                                                                                Gaps
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mus musculus in vitro fertilized eggs cDNA, RIKEN full-length enriche
library, clone:7420700M05 product:weakly similar to DJ675G8.1 (NOVEL
ZINC FINGER PROTEIN).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                           Length 341;
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SMART; SM00355; ZnF_C2H2; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 3.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 3.
SEQUENCE 341 AA; 38046 MW; 62BB9F5059125A2B CRC64;
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PROSITE; PS50157; ZINC FINGER C2H2 2; 3.
SEQUENCE 341 AA; 38073 MW; AC8ZD4C0472B054C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                             17;
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                                                                                                                        Score 56; DB 2;
Pred. No. 37;
                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                 27.9%; Score 56; DB 2; 29.4%; Pred. No. 37;
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                                                                                                                                                                             7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             341 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequen
01-OCT-2003 (TrEMBLrel. 25, Last annota
Germ cell specific zinc finger protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=129/Sv x C57BL; TISSUE=Testis;
MEDLINE=22239718; PubMed=12351194;
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GO; GO:0007276; P:gametogenesis; IDA.
InterPro; IPR007087; Znf_C2H2.
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ProDom; PD000003; Znf C2H2; 2.
SMART; SM00355; ZnF C2H2; 3.
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EMBL, AF508984; AAN31656.1; -.
HSSP; P08047; 1SP1.
                                                                                                                              27.98;
                                                                                                                                                        29.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=Zfp393; Synonyms=Gzf;
Mus musculus (Mouse).
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                                                                                                                                                                          10; Conservative
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Matches
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C STRAIN-CSTBL/61, TISSUE-In vitro fertilized eggs;
A dachi J. Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
A Managaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                               the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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ProDom; PD000003; Znf C2H2; 2.

SMART; SM0355; ZnF CZH2; 3.

PROSITE; PS00028; ZINC FINGER C2H2 1; 3.

PROSITE; PS50107; ZINC FINGER C2H2 2; 3.

SEQUENCE 341 AA; 38094 MW; A332DB7FE231AFFC CRC64;
STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs; MEDLINE=99279253; PubMed=10349636; Carninci P., Hayashizaki Y.; Hidh-efficiency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                STRAIN=CS7BL/6J; TISSUE=In vitro fertilized eggs;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=In vitro fertilized eggs; The FANTOM Consortium,
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GO; GO:0007276; P:gametogenesis; IDA.
Interpro; IPR007087; Znf C2H2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 420:563-573(2002)
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Best Local Similarity
Matches 10; Conserv
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Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Senopus laevis (African clawed frog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straubberg R.; Straubberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC064748; AAH64748.1; ... SEQUENCE 341 AA; 38046 MW; 62BB8F5059125A2B CRC64;
                                                                                                                                      Last sequence update)
Last annotation update)
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                         CNEREWESQLIRSLPEHGVRCPSQLAPIPFONYC 93
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STRAIN=C57BL/6J; TISSUE=Unfertilized egg;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
                                                                                                                          Created)
                                                                                                                     01-JUN-2004 (TrEMBLrel. 27, 01-JUN-2004 (TrEMBLrel. 27, 01-JUN-2004 (TrEMBLrel. 27,
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                                                                                                PRELIMINARY;
                                                                                                                                                                  Zinc finger protein 393.
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                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                AAH64748
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                                                                                                                                                            initiative.
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Riausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Abramson R.D., Mullahy S.J.,
Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muxny D.M., Sodergren B.J., Lu K., Gibbs R.A.,
Willalon D.K., Muxny D.M., Sodergren B.J., Lu K., Gibbs R.A.,
Willianon D.K., Muzny D.M., Sodergren B.J., Lu K., Gibbs R.A.,
Willian A., Youchman J.W., Schwyten B.D., Dickson M.C.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Green E.D., Marra M.A.,
A Green S.J., Marra M.A.,
Redriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Wenneration and initial analysis of more than 15,000 full-length human
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                         E., Sive H.L.;
databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.9%; Score 56; DB 2; Length 387;
25.4%; Pred. No. 42;
tive 6; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387 AA; 42066 MW; 1A386A239C7C8A82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                   Hick E., Sun B.I., Collins-Racie L., Lavallie Submitted (FEB-1999) to the EMBL/GenBank/DDBJ (EMBL, AF131890; AAD$4072.1; -. AP131890; AAD$4072.1; -. AP0174; INGR. (GO; GO:0016021; C:integral to membrane; IEA. (GO; GO:0004872; F:receptor activity; IEA. (GO; GO:0001672; F:receptor activity; IEA. (GO; GO:0007162; P:signal transduction; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            392 AA
                                                                                                                                                                                                      InterPro; IPR0016488; Death.
InterPro; IPR011029; DEATH_like.
InterPro; IPR011029; DEATH_like.
InterPro; IPR011368; TNFR_c6.
Pfam; PF00531; DEATH; 1.
Pfam; PF00020; TNFR c6; 4.
SWART; SW00005; DEATH; 1.
PROSITE; PS50017; DEATH; 1.
PROSITE; PS50050; TNFR; 4.
PROSITE; PS50050; TNFR NGFR_1; UNKNOWN_3.
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MEDLINE=22388257; PubMed=12477932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 25.4 tes 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane
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Matches
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108 CPERQYLDS-NGICLPCQLCSKGHGVVSQCTHNKNTVCQLCSSGFYSBVKSSBSPCLPCR 166
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30; Gaps
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
Xenopodinae, Xenopus, Xenopus.
MEDLINE=22341132; PubMed=12454917; Medines J., Clifton S.W., Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; Clore to P.; Richardson P.; Richardson P.; Medenetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S.L., Straueberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.9%; Score 56; DB 2; Length 392; 25.4%; Pred. No. 43;
                                                                                                                                                                                                       Klein S., Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BC068640; AAH68640.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 AA; 42538 MW; 0B41CED6CCE080FB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Mismatches
                                                                                                                                                                                                                                                                                                                                          Pfam; PF00531; Death; 1.
Pfam; PF00020; TNFR_c6; 4.
SMART; SM00005; DEATH; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50017; DEATH DOMAIN; 1.
PROSITE; PS50050; TNFR NGFR 1; UNKNOWN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-WAY-2004 (TrEMBLrel. 27, Created)
10-WAY-2004 (TrEMBLrel. 27, Last seq
10-WAY-2004 (TrEMBLrel. 27, Last ann
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                          Interpro; IPR000488; Death.
Interpro; IPR011029; DEATH like.
Interpro; IPR001368; TNFR_G6.
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                                                                                                                  Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      initiative.";
Dev. Dyn. 225:384-391(2002).
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Aatches 16; Conservative
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DOMAIN
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     3,
                                                                                                                                                                                                                                                                                                                                                                108 CPERQYLDS-NGICLPCQLCSKGHGVVSQCTHNKNTVCQLCSSGFYSEVKSSESPCLPCR 166
                                                                                                                                                                                                                                                                                                                                                --SSNTPPLTCQ 31
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKenan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A sperm membrane protein that binds in a species-specific manner to the egg extracellular matrix is homologous to von Willebrand factor."; J. Biol. Chem. 270:26028 (1995).
-!- FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the spical region of the sperm head (FB similarity).

TISSUE SPECIFICITY: In testis, primarily in haploid spermatids. Not in lung, liver, heart, spleen, brain, kidney, epididymis. DOWAIN: The MAM domains probably mediate sperm adhesion to the zona pollucida.

DOWAIN: During sperm migration through the reproductive tracts, the muchin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.
                                                                                                                                                                                                                                                                                                                         30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 823-830; 859-872; 883-890; 920-925; 960-967; 1235-1244; 1349-1354; 1518-1532; 1624-1656; 1658-1667; 1777-1795 AND 1914-1921.
STRAIN=Meishan; TISSUE-Testis; MEDLINE=96064658; PubMed=7592795;
                                                                                                                                                                                                                                                                                               2; Length 392;
                                                                                                                                                                                                                                                                                            27.9%; Score 56; DB 2; Length 392
25.4%; Pred. No. 43;
tive 6; Mismatches 11; Indels
                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-Embryo;
KIein S., Strausberg R.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC066640; AH66840.1; -.
                                                                                                                                                                                                                                                                     SEQUENCE 392 AA; 42538 MW; OB41CED6CCE080FB CRC64;
                                                                                                                                                      and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 2476 AA.
                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHACIPCQL-----RC---
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                                                                                                                                                                                                                                                                                              Query Match 27.9
Best Local Similarity 25.4
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zonadhesin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
oligomerization (By similarity to human intestinal mucin MUC2). PTM: The MAM domains and the mucin-like domains are missing from the zonadhesin that binds to the egg extracellular matrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 X HEPTAPEPTIDE REPEATS (APPROXIMATE) (MUCIN-LIKE DOMAIN).
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(Potential).
(Potential).
(Potential).
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DR PEam; PF00629; MAM; 2.

DR PEam; PF00629; MAM; 2.

DR PEam; PF01826; TIL; 5.

DR PEam; PF018245; TIL; 6.

DR PEam; PF001345; TIL; 6.

DR SMART; SM00137; MAM; 1.

DR SMART; SM001216; VWD; 4.

DR SMART; SM00216; VWD; 4.

DR SMART; SM00216; VWD; 4.

DR PROSITE; PS00022; EGF=2; 4.

DR PROSITE; PS00040; MAM=1; 1.

DR PROSITE; PS00040; MAM=1; 1.

DR PROSITE; PS00040; MAM=1; 1.

DR PROSITE; PS00060; MAM=1; 1.

DR PROSITE; PS00060; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

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DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.

DR PROSITE; PS000740; MAM=1; 1.
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                                                                         Processing might occur during sperm maturation and/or
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(GlcNAc.
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VWFD 2.
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By similarity.
By similarity.
By similarity.
Ny similarity.
                                                                                                                 SIMITARITY: Contains 1 EGF-like domain. SIMILARITY: Contains 2 MAM domains. SIMILARITY: Contains 5 VWFD domains.
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InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF_
InterPro; IPR000998; MAM.
InterPro; IPR000198; MID Cysrich.
InterPro; IPR0001007; WWF_C
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VWFD 4.
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                                                                                                capacitation.
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EMBL; AB030968; BAB11770.1; GenBank/DDBJ databases.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0019028; C:viral capsid; IEA.

GO; GO:0005198; F:structural molecule activity; IEA.

InterPro; IPR002519; HCV_env.

Pfam; PF01539; HCV_env. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; seRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                     (Potential)
                                                                                                                                                         (Potential)
                                                                                                                                                                                                                                                                                                                                                                                     4;
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                                                                                                                                                                           C -> V (in Ref. 1; AA sequence).
S -> Y (in Ref. 1; AA sequence).
W -> Y (in Ref. 1; AA sequence).
S -> K (in Ref. 1; AA sequence).
Mw; A13B690375A6548C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 146;
                                                                                                                                                                                                                                                                                                                               27.9%; Score 56; DB 1; Length 2476; 31.6%; Pred. No. 2.9e+02; ive 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coat protein; Envelope protein; Glycoprotein; Polyprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 AA; 15763 MW; 9C67046FD8507C30 CRC64;
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N-linked (GlCNAC. ..)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 AA
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(TrEMBLrel. 16, L
(TrEMBLrel. 24, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.6%;
31.8%;
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01-MAY-2000 (TrEMBLrel. 13,
05-JUL-2004 (TrEMBLrel. 27,
CG7714-PA (RH24988p).
                                                                                                                                                                                                                                                                                                                                                      Local Similarity 31.6
les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Conservative
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Best Local Similarity
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                                                      CARBOHYD
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OK REPHYGLOGAE, TO CROSOPHILIDGE, DECORPHILA,

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REALLE-2118-COL F. CAILLER S. E. HOLK R. A. HOWKINS R. A., Godayne J. D.,

RADINE-2118-COL F. CAILLER S. E. HOLK R. A., SHADKINS R. A., GOLDER S. R.,

REALLER-2118-COL F. CAILLER S. E. HOLK R. A., SHADKINS R. A., GOLDER S. R.,

RADINE-2118-COL F. CAILLER S. E. S. HOLK R. A., SHADKINS R. A., GOLDER S. R.,

RADINE S. SHADKON R. A. RADINE S. E. HOLK R. A., SHADKINS R. A., GOLDER S. R.,

RADINE S. C. CAILLER S. E. SHADKER S. C. C. REPERS C. C. REPERS C. D.,

RADINE S. C. BORDHAN R. A. A. H. J., ANDIVES FERRINGCH L., Balbakov S. A.

RADINE K. A. BORDHAN R. A. BORN S. BRANKARDON D., BOLDHAROV S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. BANDKON S. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. BANDKON S. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. BANDKON S. C. BANDKON S. C. BANDKON S. BANDKON S. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. S. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BANDKON S. C. BA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                        "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Liu J., Li X., Tufan S.N.L., Clayton M., Wu M.,
Lian Z., Liu J., Li L., Li X., Tufan S.N.L., Clayton M., Wu M.,
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY202325, AA047666.1, -.
InterPro; IPR001304; Lectin C.
InterPro; IPR001304; Lectin C.
InterPro; IPR001007; WWF_C.
SMART; SM00214; VWC; 6.
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Application Applic

Application US/09854864

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GENERAL INFORMATION:
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APPLICANT: THEILL, LARS EYDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: 2001-09-11
CURRENT APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-13
PRIOR FILING DATE: 2000-05-13
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Best Local Similarity 100.0
Matches 34; Conservative
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US-09-854-864-21
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US-09-854-864-5
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APPLICANT: THELL, LARS EXDE
APPLICANT: THELL, LARS EXDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/00/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO
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                                                     ALIGNMENTS
                                                                                                                                                                                                                                                Sequence 7, Application US/09854864
Patent No. 6774106
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US-09-854-864-6
; Sequence 6, Application US/09854864
; Batent No. 6774106
; GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-854-864-7
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; ORGANISM: Homo sapiens
US-09-854-864-6
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Best Local Similarity
Matches 34; Conserv
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Matches 34; Conserv
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Gaps

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Length 58 Indels

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Sequence 13, Application US/09854864

Batent No. 6774106

GENERAL INFORMATION:
FOR THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

TITLE OF INVENTION:
FILE REFERENCE: A-686B

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT APPLICATION NUMBER: US 60/214,039

PRIOR PAPLICATION NUMBER: US 60/214,039

PRIOR PAPLICATION NUMBER: US 60/214,591

PRIOR PAPLICATION NUMBER: US 60/214,591

PRIOR PILING DATE: 2000-06-12

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 13

LENGTH: 81

LENGTH: 81
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Patent No. 6774106

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, TITLE OF INVENTION: BLYS/AGP-3, AND TACI
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100.0%; Pred. No. 5.9e-17;
tive 0; Mismatches 0;
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RESULT 3 US-09-854-864-21

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Sequence 11, Application US/09854864

Patent No. 6774106

GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
FILE OF INVENTION:
FILE REFERENCE: A-6868

CURRENT PAPLICATION WHMBER: US/09/854,864

CURRENT PILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-05-12

PRIOR PILING DATE: 2000-05-13

PRIOR FILING DATE: 2000-05-13

PRIOR FILING DATE: 2000-05-13

PRIOR PILING DATE: 2000-05-13

PRIOR PILING DATE: 2000-05-13

PRIOR PILING DATE: 2000-05-13

SOFTWARE: PatentIn version 3.1

SEQ ID NO 11

LENGTH: 185

LENGTH: 185
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TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 2979-72
CURRENT APPLICATION NUMBER: US/09/565,423
CURRENT PILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,892
PRIOR PILING DATE: 2000-05-01
PRIOR PILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 17.
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Best Local Similarity 70.6%; Pred. No. 6.4e-09;
Matches 24; Conservative 2; Mismatches 6;
                                                                                                                                Query Match
100.0%; Score 201; DB 4;
Best Local Similarity 100.0%; Pred. No. 2e-16;
Matches 34; Conservative 0; Mismatches 0;
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; Sequence 17, Application US/09565423;
; Eatent No. 6475987;
; GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.1 SEQ ID NO 9 LENGTH: 283 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Mus musculus
US-09-565-423-17
                                                                       ; ORGANISM: Homo sapiens
US-09-854-864-9
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APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS EXDE
APPLICANT: TYU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: METHORS AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-27
NUMBER OF SEQ ID NOS: 31
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Pred. No. 1.3e-16;
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                                                                                                                                                                                                                                                                                                                         0; Mismatches
                 CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILLING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILLING DATE: 2000-05-12
PRIOR PILLING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SEQ ID NO 5
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Patent No. 6774106
GENERAL INFORMATION:
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US-09-565-423-11
                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
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Best Local Similarity
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US-09-854-864-9
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Sequence 16, Application US/09854864

Sequence 16, Application US/09854864

Sequence 16, Application US/09854864

GENERAL INFORMATION:
APPLICANT: THEILL, LARS EYDE

APPLICANT: TU, GANG

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: METHODS AND TACI
FILE REPERBACE: A-6868

CURRENT APPLICATION NUMBER: US/09/854,864

CURRENT PILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-05-12

PRIOR PAPLICATION NUMBER: US 60/214,591

PRIOR PILING DATE: 2000-06-27

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 16

LENGTH: 67

LENGTH: 67
                                                                                                                                      APPLICANT: THEILL, LARS EVDE
APPLICANT: THEILL, LARS EVDE
APPLICANT: THEILL, LARS EVDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENTING DATE: 2000-06-27
TYPE: PRI
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Pred. No. 0.35;
8; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66.5;
Pred. No. 0.
                                                                     Sequence 20, Application US/09854864 Patent No. 6774106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 33.1%;
Best Local Similarity 32.4%;
Matches 11; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 33.1%;
Best Local Similarity 32.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens US-09-854-864-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                       GENERAL INFORMATION:
                                                    -09-854-864-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-854-864-16
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                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS EXDE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT FILING DATE: 2001-09-11
PRIOR PPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SSPTWARE: PATENTIAN OF SEQ ID NOS: 31
SSPTWARE: PATENTIAN OF SEQ ID NOS: 31
SSPTWARE: PATENTIAN OF SEQ ID NOS: 31
SSPTWARE: PATENTIAN OF SEQ ID NOS: 31
LENGTH: 281
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REPERENCE: A-686B
CURRENT PELLON NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-06-7
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATENT NESS OF SEQ ID NOS: 31
SOFTWARE: PATENT NESS OF SEQ ID NOS: 31
SOFTWARE: PATENT NESS OF SEQ ID NOS: 31
SOFTWARE: PATENT NESS OF SEQ ID NOS: 31
                             ä
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 67.7%; Score 136; DB 4; Length 281; Best Local Similarity 70.6%; Pred. No. 9.6e-09; Matches 24; Conservative 2; Mismatches 6; Indels
                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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69.7%; Pred. No. 0.00044;
tive 1; Mismatches 2;
70.6%; Pred. No. 6.4e-09; tive 2; Mismatches 6
                                                                        1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                   5 CFHSEYFDSLLHACKPCHLRCSN--PPATCQPYC 36
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                                                                                                                                                                                                                                    Sequence 10, Application US/09854864
Patent No. 6774106
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Patent No. 6774106
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: human-murine Consensus
                      24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Mus musculus
US-09-854-864-10
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Best Local Similarity
  Best Local Similarity
                                                                                                                                                                                          RESULT 10
US-09-854-864-10
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                        Matches
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AFFILTON. VON BULOW, GOLZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/290,333

FILING DATE: 12-Apr-1999

CLASSIFICATION: «Inchown»

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esg., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET WINBER: 1340-1-007 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14-Feb-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
PRILING DATE: «Unknown»
ATTONBEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09782857A Patent No. 6500428 GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
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TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLBIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 166;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
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                                                                                          NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: ISM FOC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,572A
FILING DATE: 28-FEB-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 1340-1-007
TELECOMMUTCATION INFORMATION:
TELEPHONE: 201-487.5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : : | : | : | : | : | : | : | : | 34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Patent No. 6316222
GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THEREOF
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STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acid
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US-08-810-572A-6
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STRANDEDNESS: single
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APPLICANT: AND Richard J.
APPLICANT: BUIOW, GOEZ
VON BUIOW, GOEZ
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWMER: Patentin Release #1:0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/290,333
                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION UNMER:
FILING DATE: 28 FFEB 1997
CLASSIFICATION: 536
ATTOWNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAN: 201-447-5800
TELEFRAN: 201-447-5800
TELEFRAN: 201-447-5800
TELEFRAN: 201-447-5800
TELEFRAN: 201-447-5800
TELEFRAN: 201-447-5800
TELEFRAN: 201-447-5800
TELEFRAN: 201-447-5800
TELEFRAN: 201-543-1644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007 PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-Apr-1999
CLASSIFICATION: <Unknown>
                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09290333; Patent No. 6316222
GENERAL INFORMATION:
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                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
New Jersey
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APPLICANT: THEILL, LARS EYDE
APPLICANT: YU, GANG
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
FILE REFERENCE: A-686B
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR APPLICATION NUMBER: US 60/204,039
PRIOR FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/214,591
PRIOR FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHIN Version 3.1
SOFTWARE: PATCHIN Version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Bram, Richard J.
APPLICANT: von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
33.1%; Score 66.5; DB 4; Length 166;
Best Local Similarity 32.4%; Pred. No. 0.96;
Matches 11; Conservative 8; Mismatches 14; Indels 1
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
TYPE: amino acid
STRANDEDNESS: single
STRANDEDNESS: single
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08810572A
Patent No. 5969102
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Patent No. 6774106
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                 FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 32.4%
Best Local 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: Floor
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                           US-09-782-857A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-854-864-15
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based
TITLE OF INVENTION: Thereon
TITLE OF INVENTION: Thereon
CURRENT APPLICATION NUMBER: US/09/848,295
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,193
PRIOR PILING DATE: 2000-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Yu. Guo-Liang, et al.
TITLE OF INVENTION:
CURRENT APPLICATION WINDER: US/09/879,919
CURRENT APPLICATION NUMBER: US/09/879,919
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR APPLICATION NUMBER: 60/277,978
PRIOR PILING DATE: 2001-03-23
PRIOR PILING DATE: 2001-03-13
PRIOR PILING DATE: 2000-10-13
PRIOR PILING DATE: 2000-10-33
PRIOR PILING DATE: 2000-10-33
PRIOR PILING DATE: 2000-10-33
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/241,952
PRIOR PILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/241,537
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR APPLICATION NUMBER: 60/016,812
PRIOR PILING DATE: 1997-031-14
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN Ver. 2.1
LENGRHY: 293
                                                                                                                                                                                                         Length 293;
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                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                     Query Match 33.1%; Score 66.5; DB 4; Best Local Similarity 32.4%; Pred. No. 1.7; Matches 11; Conservative 8; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                           34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
                                                                                                                                                                                                                                                                                                                                                                               1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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                                       ORGANISM: Homo sapiens;
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-782-857A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22, Application US/09879919
Patent No. 6541224
GENERAL INFORMATION:
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Patent No. 6623941
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SOFTWARE: Patentin Ver. 2.1
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ORGANISM: Homo sapiens
    ORIGINAL SOURCE:
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US-09-848-295-4
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TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
CAML, WUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
33.1%; Score 66.5; DB 3; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,857A
FILING DATE: 14 Feb-2001
CLASSIPICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :: | | | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1340-1-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
WOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09782857A Patent No. 6500428 GENERAL INFORMATION:
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TELEPHONE: 201-487-5800
TELECOMMUNICATION INFORMATION TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 293 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bram, Richard J.
                                                                          TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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COUNTRY: USA
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US-09-782-857A-2
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APPLICANT: Hardy, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of
TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2476;
                                  Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/276,967
FILING DATE: Submitted Herewith
CLASSIFICATION: 530
ATTONNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REGISTRATION NUMBER: 33,928
TELEFRENCE/DOCKET NUMBER: UTSD:418\KIT
TELEFRENCE/TON INFORMATION:
TELEFRENCE: 713-787-1400
TELEFRAX: 713-789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1851 CSAHSVYTSCVPSCLPSCODPEGOCTGAGAPSTCEEGC 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHACIP-CQ---LRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
                                14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.9%; Score 56; DB 2; I ilarity 31.6%; Pred. No. 2.3e+02; Conservative 8; Mismatches 14;
                                                                             1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
                                                                                                        34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
       Similarity 32.4%; Pred. No. 2.2; 11; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-621-976-6330

Sequence 6330, Application US/09621976

; Patent No. 6639063

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                             Sequence 2, Application US/08276967; Patent No. 5851817; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2476 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
       Best Local Similarity
Matches 11; Conserv
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                         US-08-276-967-2
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Patent No. 6774106

GENERAL INFORMATION:

APPLICANT: THEILL, LARS EYDE

APPLICANT: THEILL, LARS EYDE

APPLICANT: TY, GANG

TILLE OF INVENTION: BLYS/AGP-3, AND TACI

TILLE OF INVENTION: BLYS/AGP-3, AND TACI

TILLE OF INVENTION: MUMBER: US/09/854,864

CURRENT FILING DATE: 2001-09-11

PRIOR PILING DATE: 2000-05-12

PRIOR FILING DATE: 2000-06-12

PRIOR FILING DATE: 2000-06-17

PRIOR FILING DATE: 2000-06-27

WHERE APPLICATION NUMBER: US 60/214,591

PRIOR FILING DATE: 2000-06-27

WHERE APPLICATION NUMBER: 31

SOFTWARE: Patentin version 3.1

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: THEILL, LARS EXDE
APPLICANT: THEILL, LARS CAPE
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,
TITLE OF INVENTION: BLYS/AGP-3, AND TACI
CURRENT APPLICATION NUMBER: US/09/854,864
CURRENT FILING DATE: 2001-09-11
PRIOR PPLICATION NUMBER: US 60/204,039
PRIOR PILING DATE: 2000-05-12
PRIOR PILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PATCHTIN VETSION 3.1
SSOFTWARE: PATCHTIN VETSION 3.1
LENGTH 293
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                                                                                                                                           Query Match
33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

33.1%; Score 66.5; DB 4; Length 293;
Best Local Similarity 32.4%; Pred. No. 1.7;
Matches 11; Conservative 8; Mismatches 14; Indels 3
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                                                                                                                                                                                                                                          1 CSONEYFDSLLHACIPCOLRCSSNTPPLTCQRYC 34
                                                                                                                                                                                                                                                                      34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 CPEEQYWDPLLGTCMSCKTICNHQS-QRTCAAFC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CSQNEYFDSLLHACIPCQLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/09854864
Patent No. 6774106
                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-295-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                      US-09-854-864-14
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TYPE: PRT
ORGANISM: Hon
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SEQ ID NO 4
LENGTH: 293
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Sequence 2, Application US/09848295

Batent No. 6623941

GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Baker, Kevin
APPLICANT: Ruben, Steven M.
TITLE OP INVENTION: Thereon
TITLE OP INVENTION: Thereon
FILE REPERBNCE: PFS27
CURRENT APPLICATION NUMBER: US/09/848,295
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,193
PRIOR FILING DATE: 2000-05-05
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                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: MORIKAWA, MINORU
APPLICANT: HARADA, NAOKI
APPLICANT: HARADA, NAOKI
TITLE OF INVENTION: GENE ENCODING IGG FC REGION-BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: PO BOX 747
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2733 CPÓNSHYE----LCADICSIGCSALSAPLQCPDGC 2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.6%; Score 53.5; DB 3; Best Local Similarity 34.3%; Pred. No. 9.8e+02; Matches 12; Conservative 5; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CSQNEYFDSLLHACI - PCQLRCSSNTPPLTCQRYC 34
  118 NKLFCQLAKTC-PVQLWVSSPPPPNTCVR 145
                                                                                                                        Sequence 9, Application US/08718388
Patent No. 6271362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JG, GERALD M
RECISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
INFORMATION FOR SEO ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 142
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-718-388-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                               CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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US-09-848-295-2
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Sequence 25721, Application US/09252991A

Sequence 25721, Application US/09252991A

Sequence 25721, Application US/09252991A

Sequence 25721, Application US/09252991A

SERENT NOTIFIED OF INVERTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVERTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVERTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT PELLING DATE: 1999-02-18

PRIOR PILLING DATE: 1998-02-18

PRIOR PILLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQUENCE: APPLICATION NUMBER: US/09/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 54; DB 4; Length 431;
Pred. No. 73;
3; Mismatches 5; Indels
                                                                                                                                                                         Score 54; DB 4; Length 98;
Pred. No. 17;
                                                                                                                                                                                                                          Indels
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Fatent No. 6307036
GENERAL INFORMATION:
APPLICANT: Yorkshire Cancer Research
TITLE OF INVENTION: Tumour Suppressor Gene
FILE REFERENCE: Canine p53
CURRENT FILING DATE: 1999-02-25
FRIOR APPLICATION NUMBER: 9804178.3
FRIOR APPLICATION NUMBER: 9804178.3
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 381
                                                                                                                                                                                                                          4; Mismatches
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                                                                                                                                                                                                                                                                      14 CIPCQLRCSSNTPPLTCQRYC 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) OKCANISM: Pseudomonas aeruginosa
US-09-252-991A-25721
                                                                                                                                                                       Query Match
Best Local Similarity 38.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.9%;
Best Local Similarity 50.0%;
Matches 10; Conservative
                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-09-621-976-6330
SOFTWARE: Patent.pm
SEQ ID NO 6330
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Canis
US-09-257-580-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 28
US-09-257-580-2
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Gaps

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APPLICANT: Abulh, Alejandro
APPLICANT: Abulh, Alejandro
APPLICANT: Abulh, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6455632e1 Human Phosphatases and Polynucleotides Encoding the
FILE REFERENCE: LEX-0189-USA
FURENT APPLICATION NUMBER: US/09/877,730
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR APPLICATION NUMBER: US 60/210,607
NUMBER OF SEO ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Abuin, Alejandro.
APPLICANT: Abuin, Alejandro.
APPLICANT: Sands Arthur T.
TITLE OF INVENTION: No. 645632el Human Phosphatases and Polymucleotides Encoding the TILE OF INVENTION: LEX-0189-USA
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT PILING DATE: 2001-06-08
FRIOR APPLICATION NUMBER: US 60/210,607
RIOR PAPLICATION NUMBER: US 60/210,607
RIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Indels
     Best Local Similarity 33.3%; Pred. No. 1.8e+02; Matches 10; Conservative 6; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 52; DB 4;
Pred. No. 2.1e+02;
6; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.9%; Score 52; DB 4; 33.3%; Pred. No. 2.4e+02; ive 6; Mismatches 14.
                                                                                                                            580 NSFIDAKVLSCGICCISRSSIPPPCVCKMY 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 NEYFDSLLHACIPCOLRCSSNTPPLTCORY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 NEYFDSLLHACIPCQLRCSSNTPPLTCQRY 33
                                                                                                                                                                                                                                              Sequence 22, Application US/09877730 Patent No. 6465632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/09877730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.3%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: homo sapiens
US-09-877-730-22
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US-09-877-730-16
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Best Local Similarity
Matches 10; Conserv
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US-09-877-730-16
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LENGTH: 712
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# FACELIA NO. 190303.2.
# APPLICANT: Walke, D. Wade
# APPLICANT: Walke, D. Wade
# APPLICANT: Scoville, John
# APPLICANT: Turner, C. Alexander Jr.
# APPLICANT: Turner, C. Alexander Jr.
# APPLICANT: Sands, Arbur T.
# APPLICANT: Sands, Arbur T.
# APPLICANT: Sands, Arbur T.
# TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polymucleotides Encoding the
# PILOR REPEIRANCE: LEST-0189-105A
# CURRENT APPLICATION NUMBER: US 60/210,607
# PRIOR APPLICATION NUMBER: US 60/210,607
# PRIOR PILING DATE: 2000-06-09
# NUMBER OF SEQ ID NOS: 31
# SOFTWARE: FastSEQ for Windows Version 4.0
# SEQ ID NOS: 31
# SEG THE SEC TO WINDOWS TO TAYE: PRT
# TYPE: PRT
# TYPE: PRT
# ORGANISM: homo sapiens
# US-09-877-730-26
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APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Scoville, John
APPLICANT: Friedrich, Glann
APPLICANT: Friedrich, Glann
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6465632el Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT APPLICATION NUMBER: US 60/210,607
PRIOR APPLICATION NUMBER: US 60/210,607
                                                                                                     Ή
                                                                                                     Gaps
                                                Score 52.5; DB 4; Length 142;
Pred. No. 37;
8; Mismatches 15; Indels
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                                                                                                                                           1 CSQNEYFDSLLHACIPCOLRCSSNTPPLTCORYC 34
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 624
                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/09877730 Patent No. 6465632
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                                                Query Match 26.1%;
Best Local Similarity 29.4%;
Matches 10; Conservative
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Best Local Similarity 33.3
Matches 10; Conservative
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ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                         US-09-877-730-26
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US-09-848-295-2
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TITLE OF INVENTION: No. 645632el Human Phosphatases and Polymucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT APPLICATION NUMBER: US/09/877,730
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,607
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C.
COUNTRY: US.2
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PREADIN PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 NEYFDSLLHACIPCOLRCSSNTPPLTCORY 33
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Patent No. 5482928
GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: CAMMUE, BRINO PA
APPLICANT: CAMMUE, BRINO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MBER: GB 9105052.6
11-MAR-1991
                                                                                                                                                        APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
                                                                                        Sequence 2, Application US/09877730 Patent No. 6465632 GENERAL INFORMATION:
                                                                                                                                                                                                                                              Abuin, Alejandro
Zambrowicz, Brian
Sands, Arthur T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DI
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US-09-877-730-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LING DATE
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APPLICANT:
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APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
APPLICANTION: No. 6465632e1 Human Phosphatases and Polynucleotides Encoding the FILE REFERENCE: LEX-0189-USA
CURRENT APPLICATION NUMBER: US/09/877,730
PRIOR PILING DATE: 2000-06-08
PRIOR PILING DATE: 2000-06-09
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CURRENT APPLICATION NUMBER: US/09/877,730

CURRENT FILING DATE: 2001-06-08

PRIOR PLILNG APPLICATION NUMBER: US 60/210,607

PRIOR PLILNG DATE: 2000-06-09

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PASLESEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH: 991
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33.3%; Pred. No. 2.8e+02;
tive 6; Mismatches 14;
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                            860 NSFIDAKVLSCGICCISRSSIPPECVCKMY 889
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NEYFDSLLHACIPCOLRCSSNTPPLTCQRY 33
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Abuin, Alejandro
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
                                                                                                                                                                                                                        APPLICANT: Walke, D. Wade
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
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                                                                                                                                                        ; Sequence 6, Application US/09877730; Patent No. 6465632
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Best Local Similarity 33.3
Matches 10; Conservative
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Matches 10, Conservative
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US-09-877-730-6
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ORGANISM: homo sapiens
                                                                                                                                                                                                       GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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Gaps
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                                                                   MOLECULE TYPE: peptide

MOLECULE TYPE: peptide

CRIGINAL SOURCE:

CRGANISH: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2

MS-08-471-329-12
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,142
FILING DATE: 20-AUG-1997
CLASSIFICATION: 800
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                                                                                                                                                                                                                                 4; Mismatches
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Best Local Similarity 38.5%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROKERERY, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESSPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-AUG-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATE: 30-AUG-1997
FILING DATE: 02-UN-1995
APPLICATION NUMBER: US 08/11,329
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 10-MAR-1992
PRIOR APPLICATION NUMBER: PCT/GB92/00423
FILING DATE: 11-MAR-1991
FILING DATE: 11-MAR-1991
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10-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105684.6
FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08915142
Patent No. 5942663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELBFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                single
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             amino acid
                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
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                           STRANDEDNESS:
                                                     TOPOLOGY:
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STREET: 1100 NEW YORK AVENUE, NW; NINTH FLOOR, EAST
STREET: TOWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               ORGANISM: FIGURE 7 AMINO ACID SEQUENCE MJ-AMP2
                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                Score 51.5; DB Pred. No. 22; 4; Mismatches
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APPLICANT: DE BOLLE, MIGUEL
APPLICANT: BROGRERRY, WILLEM F
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: CAMMUE, BRUNO PA
APPLICANT: VANDERLEYDEN, JOZEF
APPLICANT: REES, SARAH B
TITLE OF INVENTION: BIOCIDAL PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/471,329
FILING DATE: 02-JUN-1995
CLASSIPICATION: 000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,080
FILING DATE: 20-DEC-1993
APPLICATION NUMBER: PCT/GB92/00423
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 10-MAR.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105052.6
FILING DATE: 11-MAR.1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9105054.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 LLHACIPCOLRCSSNT-PPLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 MIEACIGNGGRCNENVGPPYCCSGFC 49
APPLICATION NUMBER: GB 9105684.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12, Application US/08471329
Patent No. 5689048
                  FILING DATE: 19-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELERAX: (202) 822-0944
TELERX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
TENTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-MAR-1991
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861 3000
TELERA: 671627 CUSH
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                25.6%;
38.5%;
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 38.59
Matches 10; Conservative
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                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WASHINGTON
                                                                                                                                                                                                                                                                                                                                    US-08-117-080-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 39
US-08-471-329-12
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APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: UNG 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCLODER 18, 1994
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30.158
REFERENCE/DOCKET NUMBER: 31/268
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
Sequence 40, Application US/08465380 Patent No. 5863894 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 33, Application US/08480478
Patent No. 5864009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                    ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 25.6
Best Local Similarity 29.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                 STREET: Suite 4700
CITY: LOB Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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                           DB 2; Length 63;
                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JOXIS H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTBIN
WUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :[|: | | | | | | CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                          George P. Vlasuk, Patric H. Stanssens
                      Query Match
25.6%; Score 51.5; Di
Best Local Similarity 38.5%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 4croage
COMPUTER: 1BM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 213/268
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                     10 LLHACIPCQLRCSSNT-PPLTCQRYC 34
                                                                                                                                                                  24 MIEACIGNGGRCNENVGPPYCCSGFC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08465380 Patent No. 5863894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213) 489-160
TELEFPA: (213) 955-0440
TELES: 67-3510
INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 42
US-08-465-380-40
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                                       11;
Length 77;
                                     IndelB
                                                                                                                6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                           1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                     6; Mismatches 12;
Score 51.5; DB 2;
Pred. No. 27;
                                                                                                                                                                                                                                                           GEORGE P. VLASUK; PATRICK ERIC
HUGO STANSSENS; JORIS HILDA
LIEVEN MESSENS; MARC JOZEF
LAUWEREYS; VVES RENE LAROCHE;
LAURENT STEHANE JESPERS; and
YANNICK GEORGES JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                       NEMATODE-EXTRACTED ANTI-
COAGULANT PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GANSEMAN:
TITLE OF INVENTION:
TITLE OF INVENTION:
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NUMBER OF SEQUENCES: 86

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11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 25.6%; Score 51.5; DB 2; Length 77; Best Local Similarity 29.3%; Pred. No. 27; Matches 12; Conservative 6; Mismatches 12; Indels ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 40, Application US/08486397

Patent No. 5866542

GRNERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L., Mensens, Marc J. Lauwereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yanick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum
IIILE OF INVENTION: NEMATORE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICKSKGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSQNEYFDSLLHAC --- IPCQLRCSSNTP----PLTCQRYC 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 31,269
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPHONE: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,397
FILING DATE: Unne 5, 1995
CLASSTFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZARNE L.
REFERENCE/DOCKET NUMBER: 20,158
REFERENCE/DOCKET NUMBER: 213/269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancyclostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 613 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 77 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67.3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08486397;
Patent No. 5866542;
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Goris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yors R. Laroche, Laurent S. Jespers,
APPLICANT: Yors R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT;
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CSONEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 18 Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: 1BM P.C. DOS 5.0
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,478
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 208/290
TELEPHAN: (213) 489-1600
TELEFAX: (713510
TELEFAX: (713510
TELEFAX: (713510
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IEM COMPATIBLE
OPERATING SYSTEM: IEM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                      STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-480-478-33
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                              DB 2; Length 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.6%; Score 51.5; DB 2; Length 77; 29.3%; Pred. No. 27;
                              Score 51.5; DB 2; Length 7 Pred. No. 27; 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: George P. Laroche, Laurent S. Jespers, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                           1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                          6 CGENEWLDD----CGTOKPCEAKCNEEPPEEEDPICRSRGC 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Mismatches 12;
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COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBET 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 31,270
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ); ORGANISM: Ancyclostoma caninum US-08-486-399-40
                                                                                                                                                                                                                                                                          US-08-486-399-40
; Sequence 40, Application US/08486399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                              Query Match
Best Local Similarity 29.3%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (213) 489-1600
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (213)
TELEPHONE: (213)
TELEPHONE: (213)
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Best Local Similarity 29.39
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                       Patent No. 5866543
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071
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                                                                                                                                                                                                                                                                                                                          DB 2; Length 77;
                                                                                                                                                                                                                                                                                                                     25.6%; Score 51.5; DB 2; Length 7
29.3%; Pred. No. 27;
tive 6; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys, APPLICANT: Yoris H.L. Mensens, Laurent S. Jespers, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yes R. Laroche, Laurent Matthew Moyle, APPLICANT: Peter W. Bergum
IIILE OF INVENTION: NEWATODE-EXTRACTED ANTICOAGULANT IIILE OF INVENTION: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                       1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/326,110
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY, AGENT INPORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/POCKET NUMBER: 313/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 955-0440
TELEPHONE: (213) 955-0440
TELEPHONE: 67-3510
INPORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                   ORGANISM: Ancyclostoma caninum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: 501te 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 4, Application US/08486399; Patent No. 5866543; GENERAL INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEEX: 67-3510
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.3
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                          US-08-486-397-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-486-399-4
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CITY: L
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GEORGE P. VLASUK, PATRICK ERIC APPLICANT: HUGO STANSERNS; JORIS HILDA APPLICANT: LIEVEN MESSENS; MARC JOZEF APPLICANT: LAUWERYS; YVER RENE LAROCHE; APPLICANT: TAURERYS; YVER RENE LAROCHE; APPLICANT: YANNICK GEORGES JOZEF APPLICANT: YANNICK GEORGES JOZEF APPLICANT: GANSEMANS TITLE OF INVENTION: NEWATODE-EXTRACTED ANTITITLE OF INVENTION: COAGULANT PROTEIN NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SPETWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: OCTOBER 18, 1994
ATTORNEY/AGART INFORMATION:
NAME: BTGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1000MATION:
TELECOMMUNICATION 1000MATION:
TELECOMMUNICATION 1000MATION:
TELECOMMUNICATION 1000MATION:
TELEFRONE: (213) 489-1600
TELEFRAX: (213) 955-0440
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Patent No. 5945275
GENERAL INFORMATION:
GENERAL GEORGE P. VLASUK; PATRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Ancyclostoma caninum
                            STREET: 633 West Fifth Street STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 67.3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
     ADDRESSEE: Lyon &
                                                                             Los Angeles
California
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STATE: California
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                                                                                                                                 U.S.A.
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                                                                             STATE: Call
COUNTRY: U.S
90071
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US-08-326-110A-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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                                         GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yes R. Laroche, Laurent S. Jespers,
APPLICANT: Yes R. Laroche, Laurent S. Jespers,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
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APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CSQNEYFDSLLHAC---IPCQLRCSSNTP----PLTCQRYC 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 CGENEWLDD----CGTQKPCEAKCNEEPPEEEDPICRSRGC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.6%; Score 51.5; Di 29.3%; Pred. No. 27; Itive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION S30
PRIOR APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODER 18, 1994
APPLICATION NUMBER: 08/326,110
FILING DATE: OCCODER 18, 1994
ATORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANDE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 30,158
TELECHONE: (213) 995-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
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Patent No. 5872098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Ancyclostoma caninum
Sequence 4, Application US/08461965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 amino acide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: George P
APPLICANT: JOALS H.J
APPLICANT: Yves R. I
APPLICANT: Yannick
APPLICANT: Peter W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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US-08-461-965-40
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Best Local Similarity 29.3%; Pred. No. 27;
Matches 12; Conservative 6; Mismatches 12; Indels 11; Gaps
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COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FatESEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/326,110A
FILING DATE: 18 OCTOBER 1994
CLASSIFICATION 530
PRIOR APPLICATION DAYA:
APPLICATION NUMBER:
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Search completed: January 28, 2005, 19:48:41 Job time : 11.0459 secs

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